SEQUENCE LISTING

<110> Schimmel, Paul
      Wakasugi, Keisuke

<120> Human Aminoacyl-tRNA Synthetase Polypeptides Useful For
      The Regulation of Angiogenesis

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<170> PatentIn Ver. 2.0

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      full-length TyrRS in pET20B

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acc cgg aac ctg cag gag gtt ctg ggg gaa gag aag ctg aag gag ata    3517
Thr Arg Asn Leu Gln Glu Val Leu Gly Glu Glu Lys Leu Lys Glu Ile
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ctg aag gag cgg gaa ctt aaa att tac tgg gga acg gca acc acg ggc    3565
Leu Lys Glu Arg Glu Leu Lys Ile Tyr Trp Gly Thr Ala Thr Thr Gly
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aaa cca cat gtg gct tac ttt gtg ccc atg tca aag att gca gac ttc    3613
Lys Pro His Val Ala Tyr Phe Val Pro Met Ser Lys Ile Ala Asp Phe
            50                  55                  60
```

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tta aag gca ggg tgt gag gta aca att ctg ttt gcg gac ctc cac gca    3661
Leu Lys Ala Gly Cys Glu Val Thr Ile Leu Phe Ala Asp Leu His Ala
            65                  70                  75
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tac ctg gat aac atg aaa gcc cca tgg gaa ctt cta gaa ctc cga gtc    3709
Tyr Leu Asp Asn Met Lys Ala Pro Trp Glu Leu Leu Glu Leu Arg Val
        80                  85                  90
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agt tac tat gag aat gtg atc aaa gca atg ctg gag agc att ggt gtg    3757
Ser Tyr Tyr Glu Asn Val Ile Lys Ala Met Leu Glu Ser Ile Gly Val
 95                  100                 105                 110
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ccc ttg gag aag ctc aag ttc atc aaa ggc act gat tac cag ctc agc    3805
Pro Leu Glu Lys Leu Lys Phe Ile Lys Gly Thr Asp Tyr Gln Leu Ser
                115                 120                 125
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aaa gag tac aca cta gat gtg tac aga ctc tcc tcc gtg gtc aca cag    3853
Lys Glu Tyr Thr Leu Asp Val Tyr Arg Leu Ser Ser Val Val Thr Gln
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cac gat tcc aag aag gct gga gct gag gtg gta aag cag gtg gag cac    3901
His Asp Ser Lys Lys Ala Gly Ala Glu Val Val Lys Gln Val Glu His
            145                 150                 155
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cct ttg ctg agt ggc ctc tta tac ccc gga ctg cag gct ttg gat gaa    3949
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Pro Leu Leu Ser Gly Leu Leu Tyr Pro Gly Leu Gln Ala Leu Asp Glu
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gag tat tta aaa gta gat gcc caa ttt gga ggc att gat cag aga aag        3997
Glu Tyr Leu Lys Val Asp Ala Gln Phe Gly Gly Ile Asp Gln Arg Lys
175                 180                 185                 190

att ttc acc ttt gca gag aag tac ctc cct gca ctt ggc tat tca aaa        4045
Ile Phe Thr Phe Ala Glu Lys Tyr Leu Pro Ala Leu Gly Tyr Ser Lys
                195                 200                 205

cgg gtc cat ctg atg aat cct atg gtt cca gga tta aca ggc agc aaa        4093
Arg Val His Leu Met Asn Pro Met Val Pro Gly Leu Thr Gly Ser Lys
                210                 215                 220

atg agc tct tca gaa gag gag tcc aag att gat ctc ctt gat cgg aag        4141
Met Ser Ser Ser Glu Glu Glu Ser Lys Ile Asp Leu Leu Asp Arg Lys
            225                 230                 235

gag gat gtg aag aaa aaa ctg aag aag gcc ttc tgt gag cca gga aat        4189
Glu Asp Val Lys Lys Lys Leu Lys Lys Ala Phe Cys Glu Pro Gly Asn
        240                 245                 250

gtg gag aac aat ggg gtt ctg tcc ttc atc aag cat gtc ctt ttt ccc        4237
Val Glu Asn Asn Gly Val Leu Ser Phe Ile Lys His Val Leu Phe Pro
255                 260                 265                 270

ctt aag tcc gag ttt gtg atc cta cga gat gag aaa tgg ggt gga aac        4285
Leu Lys Ser Glu Phe Val Ile Leu Arg Asp Glu Lys Trp Gly Gly Asn
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aaa acc tac aca gct tac gtg gac ctg gaa aag gac ttt gct gct gag        4333
Lys Thr Tyr Thr Ala Tyr Val Asp Leu Glu Lys Asp Phe Ala Ala Glu
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gtt gta cat cct gga gac ctg aag aat tct gtt gaa gtc gca ctg aac        4381
Val Val His Pro Gly Asp Leu Lys Asn Ser Val Glu Val Ala Leu Asn
            305                 310                 315

aag ttg ctg gat cca atc cgg gaa aag ttt aat acc cct gcc ctg aaa        4429
Lys Leu Leu Asp Pro Ile Arg Glu Lys Phe Asn Thr Pro Ala Leu Lys
        320                 325                 330

aaa ctg gcc agc gct gcc tac cca gat ccc tca aag cag aag cca atg        4477
Lys Leu Ala Ser Ala Ala Tyr Pro Asp Pro Ser Lys Gln Lys Pro Met
335                 340                 345                 350

gcc aaa ggc cct gcc aag aat tca gaa cca gag gag gtc atc cca tcc        4525
Ala Lys Gly Pro Ala Lys Asn Ser Glu Pro Glu Glu Val Ile Pro Ser
                355                 360                 365

cgg ctg gat atc cgt gtg ggg aaa atc atc act gtg gag aag cac cca        4573
Arg Leu Asp Ile Arg Val Gly Lys Ile Ile Thr Val Glu Lys His Pro
                370                 375                 380

gat gca gac agc ctg tat gta gag aag att gac gtg ggg gaa gct gaa        4621
Asp Ala Asp Ser Leu Tyr Val Glu Lys Ile Asp Val Gly Glu Ala Glu
            385                 390                 395

cca cgg act gtg gtg agc ggc ctg gta cag ttc gtg ccc aag gag gaa        4669
Pro Arg Thr Val Val Ser Gly Leu Val Gln Phe Val Pro Lys Glu Glu
        400                 405                 410
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ctg cag gac agg ctg gta gtg gtg ctg tgc aac ctg aaa ccc cag aag    4717
Leu Gln Asp Arg Leu Val Val Val Leu Cys Asn Leu Lys Pro Gln Lys
415             420             425             430

atg aga gga gtc gag tcc caa ggc atg ctt ctg tgt gct tct ata gaa    4765
Met Arg Gly Val Glu Ser Gln Gly Met Leu Leu Cys Ala Ser Ile Glu
                435             440             445

ggg ata aac cgc cag gtt gaa cct ctg gac cct ccg gca ggc tct gct    4813
Gly Ile Asn Arg Gln Val Glu Pro Leu Asp Pro Pro Ala Gly Ser Ala
                450             455             460

cct ggt gag cac gtg ttt gtg aag ggc tat gaa aag ggc caa cca gat    4861
Pro Gly Glu His Val Phe Val Lys Gly Tyr Glu Lys Gly Gln Pro Asp
            465             470             475

gag gag ctc aag ccc aag aag aaa gtc ttc gag aag ttg cag gct gac    4909
Glu Glu Leu Lys Pro Lys Lys Lys Val Phe Glu Lys Leu Gln Ala Asp
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ttc aaa att tct gag gag tgc atc gca cag tgg aag caa acc aac ttc    4957
Phe Lys Ile Ser Glu Glu Cys Ile Ala Gln Trp Lys Gln Thr Asn Phe
495             500             505             510

atg acc aag ctg ggc tcc att tcc tgt aaa tcg ctg aaa ggg ggg aac    5005
Met Thr Lys Leu Gly Ser Ile Ser Cys Lys Ser Leu Lys Gly Gly Asn
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att agc ctc gag cac cac cac cac cac cac tgagatccgg ctgctaacaa      5055
Ile Ser Leu Glu His His His His His His
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      full-length TyrRS in pET20B


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Glu Arg Glu Leu Lys Ile Tyr Trp Gly Thr Ala Thr Thr Gly Lys Pro
        35                  40                  45

His Val Ala Tyr Phe Val Pro Met Ser Lys Ile Ala Asp Phe Leu Lys
    50                  55                  60
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Ala Gly Cys Glu Val Thr Ile Leu Phe Ala Asp Leu His Ala Tyr Leu
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Asp Asn Met Lys Ala Pro Trp Glu Leu Leu Glu Leu Arg Val Ser Tyr
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Tyr Glu Asn Val Ile Lys Ala Met Leu Glu Ser Ile Gly Val Pro Leu
            100                 105             110

Glu Lys Leu Lys Phe Ile Lys Gly Thr Asp Tyr Gln Leu Ser Lys Glu
        115             120              125

Tyr Thr Leu Asp Val Tyr Arg Leu Ser Ser Val Val Thr Gln His Asp
    130             135             140

Ser Lys Lys Ala Gly Ala Glu Val Val Lys Gln Val Glu His Pro Leu
145             150              155                     160

Leu Ser Gly Leu Leu Tyr Pro Gly Leu Gln Ala Leu Asp Glu Glu Tyr
            165                 170                 175

Leu Lys Val Asp Ala Gln Phe Gly Gly Ile Asp Gln Arg Lys Ile Phe
            180             185              190

Thr Phe Ala Glu Lys Tyr Leu Pro Ala Leu Gly Tyr Ser Lys Arg Val
        195             200              205

His Leu Met Asn Pro Met Val Pro Gly Leu Thr Gly Ser Lys Met Ser
    210             215              220

Ser Ser Glu Glu Glu Ser Lys Ile Asp Leu Leu Asp Arg Lys Glu Asp
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Val Lys Lys Lys Leu Lys Lys Ala Phe Cys Glu Pro Gly Asn Val Glu
            245             250                     255

Asn Asn Gly Val Leu Ser Phe Ile Lys His Val Leu Phe Pro Leu Lys
        260             265              270

Ser Glu Phe Val Ile Leu Arg Asp Glu Lys Trp Gly Gly Asn Lys Thr
    275             280              285

Tyr Thr Ala Tyr Val Asp Leu Glu Lys Asp Phe Ala Ala Glu Val Val
    290             295             300

His Pro Gly Asp Leu Lys Asn Ser Val Glu Val Ala Leu Asn Lys Leu
305             310             315                     320

Leu Asp Pro Ile Arg Glu Lys Phe Asn Thr Pro Ala Leu Lys Lys Leu
            325             330             335

Ala Ser Ala Ala Tyr Pro Asp Pro Ser Lys Gln Lys Pro Met Ala Lys
            340             345             350

Gly Pro Ala Lys Asn Ser Glu Pro Glu Glu Val Ile Pro Ser Arg Leu
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Asp Ile Arg Val Gly Lys Ile Ile Thr Val Glu Lys His Pro Asp Ala
    370             375             380

Asp Ser Leu Tyr Val Glu Lys Ile Asp Val Gly Glu Ala Glu Pro Arg
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Thr Val Val Ser Gly Leu Val Gln Phe Val Pro Lys Glu Glu Leu Gln
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Asp Arg Leu Val Val Val Leu Cys Asn Leu Lys Pro Gln Lys Met Arg
        420   425   430

Gly Val Glu Ser Gln Gly Met Leu Leu Cys Ala Ser Ile Glu Gly Ile
        435   440   445

Asn Arg Gln Val Glu Pro Leu Asp Pro Pro Ala Gly Ser Ala Pro Gly
     450   455   460

Glu His Val Phe Val Lys Gly Tyr Glu Lys Gly Gln Pro Asp Glu Glu
465   470   475   480

Leu Lys Pro Lys Lys Lys Val Phe Glu Lys Leu Gln Ala Asp Phe Lys
         485   490   495

Ile Ser Glu Glu Cys Ile Ala Gln Trp Lys Gln Thr Asn Phe Met Thr
        500   505   510

Lys Leu Gly Ser Ile Ser Cys Lys Ser Leu Lys Gly Gly Asn Ile Ser
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Leu Glu His His His His His His
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          1   5   10

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Thr Arg Asn Leu Gln Glu Val Leu Gly Glu Glu Lys Leu Lys Glu Ile
 15   20   25   30

ctg aag gag cgg gaa ctt aaa att tac tgg gga acg gca acc acg ggc   3565
Leu Lys Glu Arg Glu Leu Lys Ile Tyr Trp Gly Thr Ala Thr Thr Gly
                35   40   45

aaa cca cat gtg gct tac ttt gtg ccc atg tca aag att gca gac ttc   3613
Lys Pro His Val Ala Tyr Phe Val Pro Met Ser Lys Ile Ala Asp Phe
                50   55   60

tta aag gca ggg tgt gag gta aca att ctg ttt gcg gac ctc cac gca   3661
Leu Lys Ala Gly Cys Glu Val Thr Ile Leu Phe Ala Asp Leu His Ala
            65   70   75

tac ctg gat aac atg aaa gcc cca tgg gaa ctt cta gaa ctc cga gtc   3709
Tyr Leu Asp Asn Met Lys Ala Pro Trp Glu Leu Leu Glu Leu Arg Val
        80   85   90

agt tac tat gag aat gtg atc aaa gca atg ctg gag agc att ggt gtg   3757
Ser Tyr Tyr Glu Asn Val Ile Lys Ala Met Leu Glu Ser Ile Gly Val
 95   100   105   110

```
ccc ttg gag aag ctc aag ttc atc aaa ggc act gat tac cag ctc agc    3805
Pro Leu Glu Lys Leu Lys Phe Ile Lys Gly Thr Asp Tyr Gln Leu Ser
                115                 120                 125

aaa gag tac aca cta gat gtg tac aga ctc tcc tcc gtg gtc aca cag    3853
Lys Glu Tyr Thr Leu Asp Val Tyr Arg Leu Ser Ser Val Val Thr Gln
            130                 135                 140

cac gat tcc aag aag gct gga gct gag gtg gta aag cag gtg gag cac    3901
His Asp Ser Lys Lys Ala Gly Ala Glu Val Val Lys Gln Val Glu His
        145                 150                 155

cct ttg ctg agt ggc ctc tta tac ccc gga ctg cag gct ttg gat gaa    3949
Pro Leu Leu Ser Gly Leu Leu Tyr Pro Gly Leu Gln Ala Leu Asp Glu
    160                 165                 170

gag tat tta aaa gta gat gcc caa ttt gga ggc att gat cag aga aag    3997
Glu Tyr Leu Lys Val Asp Ala Gln Phe Gly Gly Ile Asp Gln Arg Lys
175                 180                 185                 190

att ttc acc ttt gca gag aag tac ctc cct gca ctt ggc tat tca aaa    4045
Ile Phe Thr Phe Ala Glu Lys Tyr Leu Pro Ala Leu Gly Tyr Ser Lys
                195                 200                 205

cgg gtc cat ctg atg aat cct atg gtt cca gga tta aca ggc agc aaa    4093
Arg Val His Leu Met Asn Pro Met Val Pro Gly Leu Thr Gly Ser Lys
            210                 215                 220

atg agc tct tca gaa gag gag tcc aag att gat ctc ctt gat cgg aag    4141
Met Ser Ser Ser Glu Glu Glu Ser Lys Ile Asp Leu Leu Asp Arg Lys
        225                 230                 235

gag gat gtg aag aaa aaa ctg aag aag gcc ttc tgt gag cca gga aat    4189
Glu Asp Val Lys Lys Lys Leu Lys Lys Ala Phe Cys Glu Pro Gly Asn
    240                 245                 250

gtg gag aac aat ggg gtt ctg tcc ttc atc aag cat gtc ctt ttt ccc    4237
Val Glu Asn Asn Gly Val Leu Ser Phe Ile Lys His Val Leu Phe Pro
255                 260                 265                 270

ctt aag tcc gag ttt gtg atc cta cga gat gag aaa tgg ggt gga aac    4285
Leu Lys Ser Glu Phe Val Ile Leu Arg Asp Glu Lys Trp Gly Gly Asn
                275                 280                 285

aaa acc tac aca gct tac gtg gac ctg gaa aag gac ttt gct gct gag    4333
Lys Thr Tyr Thr Ala Tyr Val Asp Leu Glu Lys Asp Phe Ala Ala Glu
                290                 295                 300

gtt gta cat cct gga gac ctg aag aat tct gtt gaa gtc gca ctg aac    4381
Val Val His Pro Gly Asp Leu Lys Asn Ser Val Glu Val Ala Leu Asn
            305                 310                 315

aag ttg ctg gat cca atc cgg gaa aag ttt aat acc cct gcc ctg aaa    4429
Lys Leu Leu Asp Pro Ile Arg Glu Lys Phe Asn Thr Pro Ala Leu Lys
        320                 325                 330

aaa ctg gcc agc gct gcc tac cca gat ccc tca aag cag aag cca atg    4477
Lys Leu Ala Ser Ala Ala Tyr Pro Asp Pro Ser Lys Gln Lys Pro Met
335                 340                 345                 350
```

```
gcc aaa ggc cct gcc aag aat tca gaa cca gag gag gtc atc ctc gag    4525
Ala Lys Gly Pro Ala Lys Asn Ser Glu Pro Glu Glu Val Ile Leu Glu
            355                 360                 365

cac cac cac cac cac cac tgagatccgg ctgctaacaa agcccgaaag           4573
His His His His His His
            370

gaagctgagt tggctgctgc caccgctgag caataactag cataacccct tggggcctct  4633

aaacgggtct tgaggggttt tttgctgaaa ggaggaacta tatccggat             4682
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<210> 4
<211> 372
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: human mini
     TyrRS in pET20B

<400> 4

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Met Gly Asp Ala Pro Ser Pro Glu Glu Lys Leu His Leu Ile Thr Arg
 1               5                  10                  15

Asn Leu Gln Glu Val Leu Gly Glu Glu Lys Leu Lys Glu Ile Leu Lys
            20                  25                  30

Glu Arg Glu Leu Lys Ile Tyr Trp Gly Thr Ala Thr Thr Gly Lys Pro
        35                  40                  45

His Val Ala Tyr Phe Val Pro Met Ser Lys Ile Ala Asp Phe Leu Lys
    50                  55                  60

Ala Gly Cys Glu Val Thr Ile Leu Phe Ala Asp Leu His Ala Tyr Leu
65                  70                  75                  80

Asp Asn Met Lys Ala Pro Trp Glu Leu Leu Glu Leu Arg Val Ser Tyr
                85                  90                  95

Tyr Glu Asn Val Ile Lys Ala Met Leu Glu Ser· Ile Gly Val Pro Leu
                100                 105                 110

Glu Lys Leu Lys Phe Ile Lys Gly Thr Asp Tyr Gln Leu Ser Lys Glu
        115                 120                 125

Tyr Thr Leu Asp Val Tyr Arg Leu Ser Ser Val Val Thr Gln His Asp
    130                 135                 140

Ser Lys Lys Ala Gly Ala Glu Val Val Lys Gln Val Glu His Pro Leu
145                 150                 155                 160

Leu Ser Gly Leu Leu Tyr Pro Gly Leu Gln Ala Leu Asp Glu Glu Tyr
                165                 170                 175

Leu Lys Val Asp Ala Gln Phe Gly Gly Ile Asp Gln Arg Lys Ile Phe
            180                 185                 190

Thr Phe Ala Glu Lys Tyr Leu Pro Ala Leu Gly Tyr Ser Lys Arg Val
        195                 200                 205
```

```
His Leu Met Asn Pro Met Val Pro Gly Leu Thr Gly Ser Lys Met Ser
    210                 215             220

Ser Ser Glu Glu Glu Ser Lys Ile Asp Leu Leu Asp Arg Lys Glu Asp
225                 230             235                 240

Val Lys Lys Lys Leu Lys Lys Ala Phe Cys Glu Pro Gly Asn Val Glu
            245             250                 255

Asn Asn Gly Val Leu Ser Phe Ile Lys His Val Leu Phe Pro Leu Lys
            260             265                 270

Ser Glu Phe Val Ile Leu Arg Asp Glu Lys Trp Gly Gly Asn Lys Thr
        275             280             285

Tyr Thr Ala Tyr Val Asp Leu Glu Lys Asp Phe Ala Ala Glu Val Val
    290             295             300

His Pro Gly Asp Leu Lys Asn Ser Val Glu Val Ala Leu Asn Lys Leu
305             310             315                 320

Leu Asp Pro Ile Arg Glu Lys Phe Asn Thr Pro Ala Leu Lys Lys Leu
            325             330             335

Ala Ser Ala Ala Tyr Pro Asp Pro Ser Lys Gln Lys Pro Met Ala Lys
            340             345             350

Gly Pro Ala Lys Asn Ser Glu Pro Glu Glu Val Ile Leu Glu His His
        355             360             365

His His His His
    370


<210> 5
<211> 4100
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (3428)..(3961)

<220>
<223> Description of Artificial Sequence:  human TyrRS
      carboxyl-terminal domain in pET20B

<400> 5
tggcgaatgg gacgcgccct gtagcggcgc attaagcgcg gcgggtgtgg tggttacgcg   60

cagcgtgacc gctacacttg ccagcgccct agcgcccgct cctttcgctt tcttcccttc  120

ctttctcgcc acgttcgccg gctttccccg tcaagctcta atcgggggc tccctttagg  180

gttccgattt agtgctttac ggcacctcga ccccaaaaaa cttgattagg gtgatggttc  240

acgtagtggg ccatcgccct gatagacggt ttttcgccct ttgacgttgg agtccacgtt  300

ctttaatagt ggactcttgt tccaaactgg aacaacactc aaccctatct cggtctattc  360

ttttgattta taagggattt tgccgatttc ggcctattgg ttaaaaaatg agctgattta  420
```

```
acaaaaattt aacgcgaatt ttaacaaaat attaacgttt acaatttcag gtggcacttt 480

tcggggaaat gtgcgcggaa cccctatttg tttattttttc taaatacatt caaatatgta 540

tccgctcatg agacaataac cctgataaat gcttcaataa tattgaaaaa ggaagagtat 600

gagtattcaa catttccgtg tcgcccttat tcccttttttt gcggcatttt gccttcctgt 660

ttttgctcac ccagaaacgc tggtgaaagt aaaagatgct gaagatcagt tgggtgcacg 720

agtgggttac atcgaactgg atctcaacag cggtaagatc cttgagagtt ttcgccccga 780

agaacgtttt ccaatgatga gcacttttaa agttctgcta tgtggcgcgg tattatcccg 840

tattgacgcc gggcaagagc aactcggtcg ccgcatacac tattctcaga atgacttggt 900

tgagtactca ccagtcacag aaaagcatct tacggatggc atgacagtaa gagaattatg 960

cagtgctgcc ataaccatga gtgataacac tgcggccaac ttacttctga caacgatcgg 1020

aggaccgaag gagctaaccg cttttttgca caacatgggg gatcatgtaa ctcgccttga 1080

tcgttgggaa ccggagctga atgaagccat accaaacgac gagcgtgaca ccacgatgcc 1140

tgcagcaatg gcaacaacgt tgcgcaaact attaactggc gaactactta ctctagcttc 1200

ccggcaacaa ttaatagact ggatggaggc ggataaagtt gcaggaccac ttctgcgctc 1260

ggcccttccg gctggctggt ttattgctga taaatctgga gccggtgagc gtgggtctcg 1320

cggtatcatt gcagcactgg ggccagatgg taagccctcc cgtatcgtag ttatctacac 1380

gacggggagt caggcaacta tggatgaacg aaatagacag atcgctgaga taggtgcctc 1440

actgattaag cattggtaac tgtcagacca agtttactca tatatacttt agattgattt 1500

aaaacttcat ttttaattta aaaggatcta ggtgaagatc cttttttgata atctcatgac 1560

caaaatccct taacgtgagt tttcgttcca ctgagcgtca gaccccgtag aaaagatcaa 1620

aggatcttct tgagatcctt ttttctgcg cgtaatctgc tgcttgcaaa caaaaaaacc 1680

accgctacca gcggtggttt gtttgccgga tcaagagcta ccaactcttt ttccgaaggt 1740

aactggcttc agcagagcgc agataccaaa tactgtcctt ctagtgtagc cgtagttagg 1800

ccaccacttc aagaactctg tagcaccgcc tacatacctc gctctgctaa tcctgttacc 1860

agtggctgct gccagtggcg ataagtcgtg tcttaccggg ttggactcaa gacgatagtt 1920

accggataag cgcagcggt cgggctgaac ggggggttcg tgcacacagc ccagcttgga 1980

gcgaacgacc tacaccgaac tgagatacct acagcgtgag ctatgagaaa gcgccacgct 2040

tcccgaaggg agaaaggcgg acaggtatcc ggtaagcggc agggtcggaa caggagagcg 2100

cacgagggag cttccagggg gaaacgcctg gtatctttat agtcctgtcg ggtttcgcca 2160

cctctgactt gagcgtcgat ttttgtgatg ctcgtcaggg gggcggagcc tatggaaaaa 2220

cgccagcaac gcggcctttt tacggttcct ggccttttgc tggccttttg ctcacatgtt 2280
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ctttcctgcg ttatcccctg attctgtgga taaccgtatt accgcctttg agtgagctga 2340

taccgctcgc cgcagccgaa cgaccgagcg cagcgagtca gtgagcgagg aagcggaaga 2400

gcgcctgatg cggtattttc tccttacgca tctgtgcggt atttcacacc gcatatatgg 2460

tgcactctca gtacaatctg ctctgatgcc gcatagttaa gccagtatac actccgctat 2520

cgctacgtga ctgggtcatg gctgcgcccc gacacccgcc aacacccgct gacgcgccct 2580

gacgggcttg tctgctcccg gcatccgctt acagacaagc tgtgaccgtc tccgggagct 2640

gcatgtgtca gaggttttca ccgtcatcac cgaaacgcgc gaggcagctg cggtaaagct 2700

catcagcgtg gtcgtgaagc gattcacaga tgtctgcctg ttcatccgcg tccagctcgt 2760

tgagtttctc cagaagcgtt aatgtctggc ttctgataaa gcgggccatg ttaagggcgg 2820

ttttttcctg tttggtcact gatgcctccg tgtaaggggg atttctgttc atgggggtaa 2880

tgataccgat gaaacgagag aggatgctca cgatacgggt tactgatgat gaacatgccc 2940

ggttactgga acgttgtgag ggtaaacaac tggcggtatg gatgcggcgg gaccagagaa 3000

aaatcactca gggtcaatgc cagcgcttcg ttaatacaga tgtaggtgtt ccacagggta 3060

gccagcagca tcctgcgatg cagatccgga acataatggt gcagggcgct gacttccgcg 3120

tttccagact ttacgaaaca cggaaaccga agaccattca tgttgttgct caggtcgcag 3180

acgttttgca gcagcagtcg cttcacgttc gctcgcgtat cggtgattca ttctgctaac 3240

cagtaaggca accccgccag cctagccggg tcctcaacga caggagcacg atcatgcgca 3300

cccgtggcca ggacccaacg ctgcccgaga tctcgatccc gcgaaattaa tacgactcac 3360

tataggggaga ccacaacggt ttccctctag aaataatttt gtttaacttt aagaaggaga 3420

tatacat	atg	cca	gag	gag	gtc	atc	cca	tcc	cgg	ctg	gat	atc	cgt	gtg	3469
	Met	Pro	Glu	Glu	Val	Ile	Pro	Ser	Arg	Leu	Asp	Ile	Arg	Val	
	1				5					10					

ggg	aaa	atc	atc	act	gtg	gag	aag	cac	cca	gat	gca	gac	agc	ctg	tat	3517
Gly	Lys	Ile	Ile	Thr	Val	Glu	Lys	His	Pro	Asp	Ala	Asp	Ser	Leu	Tyr	
15					20				25						30	

gta	gag	aag	att	gac	gtg	ggg	gaa	gct	gaa	cca	cgg	act	gtg	gtg	agc	3565
Val	Glu	Lys	Ile	Asp	Val	Gly	Glu	Ala	Glu	Pro	Arg	Thr	Val	Val	Ser	
				35					40					45		

ggc	ctg	gta	cag	ttc	gtg	ccc	aag	gag	gaa	ctg	cag	gac	agg	ctg	gta	3613
Gly	Leu	Val	Gln	Phe	Val	Pro	Lys	Glu	Glu	Leu	Gln	Asp	Arg	Leu	Val	
			50					55					60			

gtg	gtg	ctg	tgc	aac	ctg	aaa	ccc	cag	aag	atg	aga	gga	gtc	gag	tcc	3661
Val	Val	Leu	Cys	Asn	Leu	Lys	Pro	Gln	Lys	Met	Arg	Gly	Val	Glu	Ser	
		65					70					75				

caa	ggc	atg	ctt	ctg	tgt	gct	tct	ata	gaa	ggg	ata	aac	cgc	cag	gtt	3709
Gln	Gly	Met	Leu	Leu	Cys	Ala	Ser	Ile	Glu	Gly	Ile	Asn	Arg	Gln	Val	
	80				85					90						

```
gaa cct ctg gac cct ccg gca ggc tct gct cct ggt gag cac gtg ttt    3757
Glu Pro Leu Asp Pro Pro Ala Gly Ser Ala Pro Gly Glu His Val Phe
 95          100             105             110

gtg aag ggc tat gaa aag ggc caa cca gat gag gag ctc aag ccc aag    3805
Val Lys Gly Tyr Glu Lys Gly Gln Pro Asp Glu Glu Leu Lys Pro Lys
            115             120             125

aag aaa gtc ttc gag aag ttg cag gct gac ttc aaa att tct gag gag    3853
Lys Lys Val Phe Glu Lys Leu Gln Ala Asp Phe Lys Ile Ser Glu Glu
                130             135             140

tgc atc gca cag tgg aag caa acc aac ttc atg acc aag ctg ggc tcc    3901
Cys Ile Ala Gln Trp Lys Gln Thr Asn Phe Met Thr Lys Leu Gly Ser
            145             150             155

att tcc tgt aaa tcg ctg aaa ggg ggg aac att agc ctc gag cac cac    3949
Ile Ser Cys Lys Ser Leu Lys Gly Gly Asn Ile Ser Leu Glu His His
    160             165             170

cac cac cac cac tgagatccgg ctgctaacaa agcccgaaag gaagctgagt        4001
His His His His
175

tggctgctgc caccgctgag caataactag cataacccct tggggcctct aaacgggtct  4061

tgaggggttt tttgctgaaa ggaggaacta tatccggat                        4100
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<210> 6
<211> 178
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: human TyrRS
      carboxyl-terminal domain in pET20B

<400> 6
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Met Pro Glu Glu Val Ile Pro Ser Arg Leu Asp Ile Arg Val Gly Lys
 1               5                  10                  15

Ile Ile Thr Val Glu Lys His Pro Asp Ala Asp Ser Leu Tyr Val Glu
            20                  25                  30

Lys Ile Asp Val Gly Glu Ala Glu Pro Arg Thr Val Val Ser Gly Leu
         35                  40                  45

Val Gln Phe Val Pro Lys Glu Glu Leu Gln Asp Arg Leu Val Val Val
    50                  55                  60

Leu Cys Asn Leu Lys Pro Gln Lys Met Arg Gly Val Glu Ser Gln Gly
 65                  70                  75                  80

Met Leu Leu Cys Ala Ser Ile Glu Gly Ile Asn Arg Gln Val Glu Pro
                85                  90                  95

Leu Asp Pro Pro Ala Gly Ser Ala Pro Gly Glu His Val Phe Val Lys
            100                 105                 110

Gly Tyr Glu Lys Gly Gln Pro Asp Glu Glu Leu Lys Pro Lys Lys Lys
        115                 120                 125
```

Val Phe Glu Lys Leu Gln Ala Asp Phe Lys Ile Ser Glu Glu Cys Ile
    130   135   140

Ala Gln Trp Lys Gln Thr Asn Phe Met Thr Lys Leu Gly Ser Ile Ser
145   150   155   160

Cys Lys Ser Leu Lys Gly Gly Asn Ile Ser Leu Glu His His His His
                165   170   175

His His

<210> 7
<211> 4682
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (3428)..(4543)

<220>
<223> Description of Artificial Sequence: human mini
      TyrRS mutant in pET20B

<400> 7
tggcgaatgg gacgcgccct gtagcggcgc attaagcgcg gcgggtgtgg tggttacgcg 60

cagcgtgacc gctacacttg ccagcgccct agcgcccgct cctttcgctt tcttcccttc 120

ctttctcgcc acgttcgccg gctttccccg tcaagctcta aatcgggggc tcccttaggg 180

gttccgattt agtgctttac ggcacctcga ccccaaaaaa cttgattagg gtgatggttc 240

acgtagtggg ccatcgccct gatagacggt ttttcgccct ttgacgttgg agtccacgtt 300

ctttaatagt ggactcttgt tccaaactgg aacaacactc aaccctatct cggtctattc 360

ttttgattta agggatttt gccgatttc ggcctattgg ttaaaaaatg agctgattta 420

acaaaaattt aacgcgaatt ttaacaaaat attaacgttt acaatttcag gtggcacttt 480

tcggggaaat gtgcgcggaa ccectatttg tttatttttc taaatacatt caaatatgta 540

tccgctcatg agacaataac cctgataaat gcttcaataa tattgaaaaa ggaagagtat 600

gagtattcaa catttccgtg tcgcccttat cccttttttt gcggcatttt gccttcctgt 660

ttttgctcac ccagaaacgc tggtgaaagt aaaagatgct gaagatcagt tgggtgcacg 720

agtgggttac atcgaactgg atctcaacag cggtaagatc cttgagagtt ttcgccccga 780

agaacgtttt ccaatgatga gcactttaa agttctgcta tgtggcgcgg tattatcccg 840

tattgacgcc gggcaagagc aactcggtcg ccgcatacac tattctcaga atgacttggt 900

tgagtactca ccagtcacag aaaagcatct tacggatggc atgacagtaa gagaattatg 960

cagtgctgcc ataaccatga gtgataacac tgcggccaac ttacttctga caacgatcgg 1020

aggaccgaag gagctaaccg cttttttgca caacatgggg gatcatgtaa ctcgccttga 1080

tcgttgggaa ccggagctga atgaagccat accaaacgac gagcgtgaca ccacgatgcc 1140

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aggatcttct tgagatcctt tttttctgcg cgtaatctgc tgcttgcaaa caaaaaaacc 1680

accgctacca gcggtggttt gtttgccgga tcaagagcta ccaactcttt ttccgaaggt 1740

aactggcttc agcagagcgc agataccaaa tactgtcctt ctagtgtagc cgtagttagg 1800

ccaccacttc aagaactctg tagcaccgcc tacatacctc gctctgctaa tcctgttacc 1860

agtggctgct gccagtggcg ataagtcgtg tcttaccggg ttggactcaa gacgatagtt 1920

accggataag cgcagcggt cgggctgaac ggggggttcg tgcacacagc ccagcttgga 1980

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ctttcctgcg ttatcccctg attctgtgga taaccgtatt accgcctttg agtgagctga 2340

taccgctcgc cgcagccgaa cgaccgagcg cagcgagtca gtgagcgagg aagcggaaga 2400

gcgcctgatg cggtattttc tccttacgca tctgtgcggt atttcacacc gcatatatgg 2460

tgcactctca gtacaatctg ctctgatgcc gcatagttaa gccagtatac actccgctat 2520

cgctacgtga ctgggtcatg gctgcgcccc gacacccgcc aacacccgct gacgcgccct 2580

gacgggcttg tctgctcccg gcatccgctt acagacaagc tgtgaccgtc tccgggagct 2640

gcatgtgtca gaggttttca ccgtcatcac cgaaacgcgc gaggcagctg cggtaaagct 2700

catcagcgtg gtcgtgaagc gattcacaga tgtctgcctg ttcatccgcg tccagctcgt 2760

tgagtttctc cagaagcgtt aatgtctggc ttctgataaa gcgggccatg ttaagggcgg 2820

ttttttcctg tttggtcact gatgcctccg tgtaaggggg atttctgttc atgggggtaa 2880

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ggttactgga acgttgtgag ggtaaacaac tggcggtatg gatgcggcgg gaccagagaa 3000

aaatcactca gggtcaatgc cagcgcttcg ttaatacaga tgtaggtgtt ccacagggta 3060

gccagcagca tcctgcgatg cagatccgga acataatggt gcagggcgct gacttccgcg 3120

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acgttttgca gcagcagtcg cttcacgttc gctcgcgtat cggtgattca ttctgctaac 3240

cagtaaggca accccgccag cctagccggg tcctcaacga caggagcacg atcatgcgca 3300

cccgtggcca ggacccaacg ctgcccgaga tctcgatccc gcgaaattaa tacgactcac 3360

tataggggaga ccacaacggt ttccctctag aaataatttt gtttaacttt aagaaggaga 3420

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tatacat atg ggg gac gct ccc agc cct gaa gag aaa ctg cac ctt atc    3469
        Met Gly Asp Ala Pro Ser Pro Glu Glu Lys Leu His Leu Ile
         1           5               10

acc cgg aac ctg cag gag gtt ctg ggg gaa gag aag ctg aag gag ata    3517
Thr Arg Asn Leu Gln Glu Val Leu Gly Glu Glu Lys Leu Lys Glu Ile
 15               20              25                  30

ctg aag gag cgg gaa ctt aaa att tac tgg gga acg gca acc acg ggc    3565
Leu Lys Glu Arg Glu Leu Lys Ile Tyr Trp Gly Thr Ala Thr Thr Gly
             35              40                  45

aaa cca cat gtg gct tac ttt gtg ccc atg tca aag att gca gac ttc    3613
Lys Pro His Val Ala Tyr Phe Val Pro Met Ser Lys Ile Ala Asp Phe
             50              55                  60

tta aag gca ggg tgt gag gta aca att ctg ttt gcg gac ctc cac gca    3661
Leu Lys Ala Gly Cys Glu Val Thr Ile Leu Phe Ala Asp Leu His Ala
             65              70                  75

tac ctg gat aac atg aaa gcc cca tgg gaa ctt cta gaa ctg cag gtc    3709
Tyr Leu Asp Asn Met Lys Ala Pro Trp Glu Leu Leu Glu Leu Gln Val
 80               85                  90

agt tac tat gag aat gtg atc aaa gca atg ctg gag agc att ggt gtg    3757
Ser Tyr Tyr Glu Asn Val Ile Lys Ala Met Leu Glu Ser Ile Gly Val
 95               100             105                 110

ccc ttg gag aag ctc aag ttc atc aaa ggc act gat tac cag ctc agc    3805
Pro Leu Glu Lys Leu Lys Phe Ile Lys Gly Thr Asp Tyr Gln Leu Ser
                 115             120                 125

aaa gag tac aca cta gat gtg tac aga ctc tcc tcc gtg gtc aca cag    3853
Lys Glu Tyr Thr Leu Asp Val Tyr Arg Leu Ser Ser Val Val Thr Gln
                 130             135                 140

cac gat tcc aag aag gct gga gct gag gtg gta aag cag gtg gag cac    3901
His Asp Ser Lys Lys Ala Gly Ala Glu Val Val Lys Gln Val Glu His
                 145             150                 155

cct ttg ctg agt ggc ctc tta tac ccc gga ctg cag gct ttg gat gaa    3949
Pro Leu Leu Ser Gly Leu Leu Tyr Pro Gly Leu Gln Ala Leu Asp Glu
                 160             165                 170
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gag tat tta aaa gta gat gcc caa ttt gga ggc att gat cag aga aag    3997
Glu Tyr Leu Lys Val Asp Ala Gln Phe Gly Gly Ile Asp Gln Arg Lys
175             180             185                 190

att ttc acc ttt gca gag aag tac ctc cct gca ctt ggc tat tca aaa    4045
Ile Phe Thr Phe Ala Glu Lys Tyr Leu Pro Ala Leu Gly Tyr Ser Lys
                195             200             205

cgg gtc cat ctg atg aat cct atg gtt cca gga tta aca ggc agc aaa    4093
Arg Val His Leu Met Asn Pro Met Val Pro Gly Leu Thr Gly Ser Lys
                210             215             220

atg agc tct tca gaa gag gag tcc aag att gat ctc ctt gat cgg aag    4141
Met Ser Ser Ser Glu Glu Glu Ser Lys Ile Asp Leu Leu Asp Arg Lys
            225             230             235

gag gat gtg aag aaa aaa ctg aag aag gcc ttc tgt gag cca gga aat    4189
Glu Asp Val Lys Lys Lys Leu Lys Lys Ala Phe Cys Glu Pro Gly Asn
        240             245             250

gtg gag aac aat ggg gtt ctg tcc ttc atc aag cat gtc ctt ttt ccc    4237
Val Glu Asn Asn Gly Val Leu Ser Phe Ile Lys His Val Leu Phe Pro
255             260             265                 270

ctt aag tcc gag ttt gtg atc cta cga gat gag aaa tgg ggt gga aac    4285
Leu Lys Ser Glu Phe Val Ile Leu Arg Asp Glu Lys Trp Gly Gly Asn
                275             280             285

aaa acc tac aca gct tac gtg gac ctg gaa aag gac ttt gct gct gag    4333
Lys Thr Tyr Thr Ala Tyr Val Asp Leu Glu Lys Asp Phe Ala Ala Glu
                290             295             300

gtt gta cat cct gga gac ctg aag aat tct gtt gaa gtc gca ctg aac    4381
Val Val His Pro Gly Asp Leu Lys Asn Ser Val Glu Val Ala Leu Asn
                305             310             315

aag ttg ctg gat cca atc cgg gaa aag ttt aat acc cct gcc ctg aaa    4429
Lys Leu Leu Asp Pro Ile Arg Glu Lys Phe Asn Thr Pro Ala Leu Lys
        320             325             330

aaa ctg gcc agc gct gcc tac cca gat ccc tca aag cag aag cca atg    4477
Lys Leu Ala Ser Ala Ala Tyr Pro Asp Pro Ser Lys Gln Lys Pro Met
335             340             345                 350

gcc aaa ggc cct gcc aag aat tca gaa cca gag gag gtc atc ctc gag    4525
Ala Lys Gly Pro Ala Lys Asn Ser Glu Pro Glu Glu Val Ile Leu Glu
                355             360             365

cac cac cac cac cac cac tgagatccgg ctgctaacaa agcccgaaag          4573
His His His His His His
                370
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```
gaagctgagt tggctgctgc caccgctgag caataactag cataacccct tggggcctct 4633

aaacgggtct tgaggggttt tttgctgaaa ggaggaacta tatccggat              4682
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<210> 8
<211> 372
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: human mini
     TyrRS mutant in pET20B

<400> 8
Met Gly Asp Ala Pro Ser Pro Glu Glu Lys Leu His Leu Ile Thr Arg
 1   5   10   15

Asn Leu Gln Glu Val Leu Gly Glu Glu Lys Leu Lys Glu Ile Leu Lys
            20   25   30

Glu Arg Glu Leu Lys Ile Tyr Trp Gly Thr Ala Thr Thr Gly Lys Pro
        35   40   45

His Val Ala Tyr Phe Val Pro Met Ser Lys Ile Ala Asp Phe Leu Lys
    50   55   60

Ala Gly Cys Glu Val Thr Ile Leu Phe Ala Asp Leu His Ala Tyr Leu
 65   70   75   80

Asp Asn Met Lys Ala Pro Trp Glu Leu Leu Glu Leu Gln Val Ser Tyr
                85   90   95

Tyr Glu Asn Val Ile Lys Ala Met Leu Glu Ser Ile Gly Val Pro Leu
            100   105   110

Glu Lys Leu Lys Phe Ile Lys Gly Thr Asp Tyr Gln Leu Ser Lys Glu
        115   120   125

Tyr Thr Leu Asp Val Tyr Arg Leu Ser Ser Val Val Thr Gln His Asp
    130   135   140

Ser Lys Lys Ala Gly Ala Glu Val Val Lys Gln Val Glu His Pro Leu
145   150   155   160

Leu Ser Gly Leu Leu Tyr Pro Gly Leu Gln Ala Leu Asp Glu Glu Tyr
                165   170   175

Leu Lys Val Asp Ala Gln Phe Gly Gly Ile Asp Gln Arg Lys Ile Phe
            180   185   190

Thr Phe Ala Glu Lys Tyr Leu Pro Ala Leu Gly Tyr Ser Lys Arg Val
        195   200   205

His Leu Met Asn Pro Met Val Pro Gly Leu Thr Gly Ser Lys Met Ser
    210   215   220

Ser Ser Glu Glu Glu Ser Lys Ile Asp Leu Leu Asp Arg Lys Glu Asp
225   230   235   240

Val Lys Lys Lys Leu Lys Lys Ala Phe Cys Glu Pro Gly Asn Val Glu
                245   250   255

Asn Asn Gly Val Leu Ser Phe Ile Lys His Val Leu Phe Pro Leu Lys
            260   265   270

Ser Glu Phe Val Ile Leu Arg Asp Glu Lys Trp Gly Gly Asn Lys Thr
    275   280   285

Tyr Thr Ala Tyr Val Asp Leu Glu Lys Asp Phe Ala Ala Glu Val Val
    290   295   300

His Pro Gly Asp Leu Lys Asn Ser Val Glu Val Ala Leu Asn Lys Leu
305   310   315   320

Leu Asp Pro Ile Arg Glu Lys Phe Asn Thr Pro Ala Leu Lys Lys Leu
          325   330   335

Ala Ser Ala Ala Tyr Pro Asp Pro Ser Lys Gln Lys Pro Met Ala Lys
      340   345   350

Gly Pro Ala Lys Asn Ser Glu Pro Glu Glu Val Ile Leu Glu His His
      355   360   365

His His His His
    370

<210> 9
<211> 5018
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (3428)..(4879)

<220>
<223> Description of Artificial Sequence: human
      full-length TrpRS in pET20B

<400> 9
tggcgaatgg gacgcgccct gtagcggcgc attaagcgcg gcgggtgtgg tggttacgcg 60

cagcgtgacc gctacacttg ccagcgccct agcgcccgct cctttcgctt tcttcccttc 120

ctttctcgcc acgttcgccg gctttccccg tcaagctcta aatcgggggc tccctttagg 180

gttccgattt agtgctttac ggcacctcga ccccaaaaaa cttgattagg gtgatggttc 240

acgtagtggg ccatcgccct gatagacggt ttttcgccct ttgacgttgg agtccacgtt 300

ctttaatagt ggactcttgt tccaaactgg aacaacactc aaccctatct cggtctattc 360

ttttgattta agggatttt gccgatttc ggcctattgg ttaaaaaatg agctgattta 420

acaaaaattt aacgcgaatt ttaacaaaat attaacgttt acaatttcag gtggcacttt 480

tcggggaaat gtgcgcggaa cccctatttg tttattttc taaatacatt caaatatgta 540

tccgctcatg agacaataac cctgataaat gcttcaataa tattgaaaaa ggaagagtat 600

gagtattcaa catttccgtg tcgcccttat ccctttttt gcggcatttt gccttcctgt 660

ttttgctcac ccagaaacgc tggtgaaagt aaaagatgct gaagatcagt tgggtgcacg 720

agtgggttac atcgaactgg atctcaacag cggtaagatc cttgagagtt ttcgccccga 780

agaacgtttt ccaatgatga gcacttttaa agttctgcta tgtggcgcgg tattatcccg 840

tattgacgcc gggcaagagc aactcggtcg ccgcatacac tattctcaga atgacttggt 900

tgagtactca ccagtcacag aaaagcatct tacggatggc atgacagtaa gagaattatg 960

cagtgctgcc ataaccatga gtgataacac tgcggccaac ttacttctga caacgatcgg 1020

aggaccgaag gagctaaccg cttttttgca caacatgggg gatcatgtaa ctcgccttga 1080

tcgttgggaa ccggagctga atgaagccat accaaacgac gagcgtgaca ccacgatgcc 1140

tgcagcaatg gcaacaacgt tgcgcaaact attaactggc gaactactta ctctagcttc 1200

ccggcaacaa ttaatagact ggatggaggc ggataaagtt gcaggaccac ttctgcgctc 1260

ggcccttccg gctggctggt ttattgctga taaatctgga gccggtgagc gtgggtctcg 1320

cggtatcatt gcagcactgg ggccagatgg taagccctcc cgtatcgtag ttatctacac 1380

gacggggagt caggcaacta tggatgaacg aaatagacag atcgctgaga taggtgcctc 1440

actgattaag cattggtaac tgtcagacca agtttactca tatatacttt agattgattt 1500

aaaacttcat ttttaattta aaaggatcta ggtgaagatc cttttttgata atctcatgac 1560

caaaatccct taacgtgagt tttcgttcca ctgagcgtca gaccccgtag aaaagatcaa 1620

aggatcttct tgagatcctt tttttctgcg cgtaatctgc tgcttgcaaa caaaaaaacc 1680

accgctacca gcggtggttt gtttgccgga tcaagagcta ccaactcttt ttccgaaggt 1740

aactggcttc agcagagcgc agataccaaa tactgtcctt ctagtgtagc cgtagttagg 1800

ccaccacttc aagaactctg tagcaccgcc tacatacctc gctctgctaa tcctgttacc 1860

agtggctgct gccagtggcg ataagtcgtg tcttaccggg ttggactcaa gacgatagtt 1920

accggataag gcgcagcggt cgggctgaac gggggggttcg tgcacacagc ccagcttgga 1980

gcgaacgacc tacaccgaac tgagatacct acagcgtgag ctatgagaaa gcgccacgct 2040

tcccgaaggg agaaaggcgg acaggtatcc ggtaagcggc agggtcggaa caggagagcg 2100

cacgagggag cttccagggg gaaacgcctg gtatctttat agtcctgtcg ggtttcgcca 2160

cctctgactt gagcgtcgat ttttgtgatg ctcgtcaggg gggcggagcc tatggaaaaa 2220

cgccagcaac gcggcctttt tacggttcct ggccttttgc tggccttttg ctcacatgtt 2280

ctttcctgcg ttatcccctg attctgtgga taaccgtatt accgcctttg agtgagctga 2340

taccgctcgc cgcagccgaa cgaccgagcg cagcgagtca gtgagcgagg aagcggaaga 2400

gcgcctgatg cggtattttc tccttacgca tctgtgcggt atttcacacc gcatatatgg 2460

tgcactctca gtacaatctg ctctgatgcc gcatagttaa gccagtatac actccgctat 2520

cgctacgtga ctgggtcatg ctgcgcccc gacacccgcc aacacccgct gacgcgccct 2580

gacgggcttg tctgctcccg gcatccgctt acagacaagc tgtgaccgtc tccgggagct 2640

gcatgtgtca gaggttttca ccgtcatcac cgaaacgcgc gaggcagctg cggtaaagct 2700

catcagcgtg gtcgtgaagc gattcacaga tgtctgcctg ttcatccgcg tccagctcgt 2760

tgagtttctc cagaagcgtt aatgtctggc ttctgataaa gcgggccatg ttaagggcgg 2820

ttttttcctg tttggtcact gatgcctccg tgtaaggggg atttctgttc atgggggtaa 2880

tgataccgat gaaacgagag aggatgctca cgatacgggt tactgatgat gaacatgccc 2940

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aaatcactca gggtcaatgc cagcgcttcg ttaatacaga tgtaggtgtt ccacagggta 3060

gccagcagca tcctgcgatg cagatccgga acataatggt gcagggcgct gacttccgcg 3120

tttccagact ttacgaaaca cggaaaccga agaccattca tgttgttgct caggtcgcag 3180

acgttttgca gcagcagtcg cttcacgttc gctcgcgtat cggtgattca ttctgctaac 3240

cagtaaggca accccgccag cctagccggg tcctcaacga caggagcacg atcatgcgca 3300

cccgtggcca ggacccaacg ctgcccgaga tctcgatccc gcgaaattaa tacgactcac 3360

tatagggaga ccacaacggt ttccctctag aaataatttt gtttaacttt aagaaggaga 3420

```
tatacat atg ccc aac agt gag ccc gca tct ctg ctg gag ctg ttc aac     3469
        Met Pro Asn Ser Glu Pro Ala Ser Leu Leu Glu Leu Phe Asn
         1               5                  10

agc atc gcc aca caa ggg gag ctc gta agg tcc ctc aaa gcg gga aat     3517
Ser Ile Ala Thr Gln Gly Glu Leu Val Arg Ser Leu Lys Ala Gly Asn
 15                  20                  25                  30

gcg tca aag gat gaa att gat tct gca gta aag atg ttg gtg tca tta     3565
Ala Ser Lys Asp Glu Ile Asp Ser Ala Val Lys Met Leu Val Ser Leu
                 35                  40                  45

aaa atg agc tac aaa gct gcc gcg ggg gag gat tac aag gct gac tgt     3613
Lys Met Ser Tyr Lys Ala Ala Ala Gly Glu Asp Tyr Lys Ala Asp Cys
             50                  55                  60

cct cca ggg aac cca gca cct acc agt aat cat ggc cca gat gcc aca     3661
Pro Pro Gly Asn Pro Ala Pro Thr Ser Asn His Gly Pro Asp Ala Thr
         65                  70                  75

gaa gct gaa gag gat ttt gtg gac cca tgg aca gta cag aca agc agt     3709
Glu Ala Glu Glu Asp Phe Val Asp Pro Trp Thr Val Gln Thr Ser Ser
     80                  85                  90

gca aaa ggc ata gac tac gat aag ctc att gtt cgg ttt gga agt agt     3757
Ala Lys Gly Ile Asp Tyr Asp Lys Leu Ile Val Arg Phe Gly Ser Ser
 95                  100                 105                 110

aaa att gac aaa gag cta ata aac cga ata gag aga gcc acc ggc caa     3805
Lys Ile Asp Lys Glu Leu Ile Asn Arg Ile Glu Arg Ala Thr Gly Gln
                 115                 120                 125

aga cca cac cac ttc ctg cgc aga ggc atc ttc ttc tca cac aga gat     3853
Arg Pro His His Phe Leu Arg Arg Gly Ile Phe Phe Ser His Arg Asp
             130                 135                 140
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atg aat cag gtt ctt gat gcc tat gaa aat aag aag cca ttt tat ctg    3901
Met Asn Gln Val Leu Asp Ala Tyr Glu Asn Lys Lys Pro Phe Tyr Leu
        145                 150                 155

tac acg ggc cgg ggc ccc tct tct gaa gca atg cat gta ggt cac ctc    3949
Tyr Thr Gly Arg Gly Pro Ser Ser Glu Ala Met His Val Gly His Leu
        160                 165                 170

att cca ttt att ttc aca aag tgg ctc cag gat gta ttt aac gtg ccc    3997
Ile Pro Phe Ile Phe Thr Lys Trp Leu Gln Asp Val Phe Asn Val Pro
175                 180                 185                 190

ttg gtc atc cag atg acg gat gac gag aag tat ctg tgg aag gac ctg    4045
Leu Val Ile Gln Met Thr Asp Asp Glu Lys Tyr Leu Trp Lys Asp Leu
                195                 200                 205

acc ctg gac cag gcc tat ggc gat gct gtt gag aat gcc aag gac atc    4093
Thr Leu Asp Gln Ala Tyr Gly Asp Ala Val Glu Asn Ala Lys Asp Ile
                210                 215                 220

atc gcc tgt ggc ttt gac atc aac aag act ttc ata ttc tct gac ctg    4141
Ile Ala Cys Gly Phe Asp Ile Asn Lys Thr Phe Ile Phe Ser Asp Leu
        225                 230                 235

gac tac atg ggg atg agc tca ggt ttc tac aaa aat gtg gtg aag att    4189
Asp Tyr Met Gly Met Ser Ser Gly Phe Tyr Lys Asn Val Val Lys Ile
        240                 245                 250

caa aag cat gtt acc ttc aac caa gtg aaa ggc att ttc ggc ttc act    4237
Gln Lys His Val Thr Phe Asn Gln Val Lys Gly Ile Phe Gly Phe Thr
255                 260                 265                 270

gac agc gac tgc att ggg aag atc agt ttt cct gcc atc cag gct gct    4285
Asp Ser Asp Cys Ile Gly Lys Ile Ser Phe Pro Ala Ile Gln Ala Ala
                275                 280                 285

ccc tcc ttc agc aac tca ttc cca cag atc ttc cga gac agg acg gat    4333
Pro Ser Phe Ser Asn Ser Phe Pro Gln Ile Phe Arg Asp Arg Thr Asp
                290                 295                 300

atc cag tgc ctt atc cca tgt gcc att gac cag gat cct tac ttt aga    4381
Ile Gln Cys Leu Ile Pro Cys Ala Ile Asp Gln Asp Pro Tyr Phe Arg
        305                 310                 315

atg aca agg gac gtc gcc ccc agg atc ggc tat cct aaa cca gcc ctg    4429
Met Thr Arg Asp Val Ala Pro Arg Ile Gly Tyr Pro Lys Pro Ala Leu
        320                 325                 330

ttg cac tcc acc ttc ttc cca gcc ctg cag ggc gcc cag acc aaa atg    4477
Leu His Ser Thr Phe Phe Pro Ala Leu Gln Gly Ala Gln Thr Lys Met
335                 340                 345                 350

agt gcc agc gac cca aac tcc tcc atc ttc ctc acc gac acg gcc aag    4525
Ser Ala Ser Asp Pro Asn Ser Ser Ile Phe Leu Thr Asp Thr Ala Lys
                355                 360                 365

cag atc aaa acc aag gtc aat aag cat gcg ttt tct gga ggg aga gac    4573
Gln Ile Lys Thr Lys Val Asn Lys His Ala Phe Ser Gly Gly Arg Asp
        370                 375                 380
```

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acc atc gag gag cac agg cag ttt ggg ggc aac tgt gat gtg gac gtg    4621
Thr Ile Glu Glu His Arg Gln Phe Gly Gly Asn Cys Asp Val Asp Val
        385                 390             395

tct ttc atg tac ctg acc ttc ttc ctc gag gac gac gac aag ctc gag    4669
Ser Phe Met Tyr Leu Thr Phe Phe Leu Glu Asp Asp Asp Lys Leu Glu
    400                 405             410

cag atc agg aag gat tac acc agc gga gcc atg ctc acc ggt gag ctc    4717
Gln Ile Arg Lys Asp Tyr Thr Ser Gly Ala Met Leu Thr Gly Glu Leu
415             420                 425                 430

aag aag gca ctc ata gag gtt ctg cag ccc ttg atc gca gag cac cag    4765
Lys Lys Ala Leu Ile Glu Val Leu Gln Pro Leu Ile Ala Glu His Gln
            435                 440                 445

gcc cgg cgc aag gag gtc acg gat gag ata gtg aaa gag ttc atg act    4813
Ala Arg Arg Lys Glu Val Thr Asp Glu Ile Val Lys Glu Phe Met Thr
            450                 455                 460

ccc cgg aag ctg tcc ttc gac ttt cag aag ctt gcg gcc gca ctc gag    4861
Pro Arg Lys Leu Ser Phe Asp Phe Gln Lys Leu Ala Ala Ala Leu Glu
        465                 470             475

cac cac cac cac cac cac tgagatccgg ctgctaacaa agcccgaaag           4909
His His His His His His
        480

gaagctgagt tggctgctgc caccgctgag caataactag cataacccct tggggcctct 4969

aaacgggtct tgaggggttt tttgctgaaa ggaggaacta tatccggat             5018


<210> 10
<211> 484
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: human
      full-length TrpRS in pET20B

<400> 10
Met Pro Asn Ser Glu Pro Ala Ser Leu Leu Glu Leu Phe Asn Ser Ile
1               5                   10                  15

Ala Thr Gln Gly Glu Leu Val Arg Ser Leu Lys Ala Gly Asn Ala Ser
            20                  25                  30

Lys Asp Glu Ile Asp Ser Ala Val Lys Met Leu Val Ser Leu Lys Met
        35                  40                  45

Ser Tyr Lys Ala Ala Ala Gly Glu Asp Tyr Lys Ala Asp Cys Pro Pro
    50                  55                  60

Gly Asn Pro Ala Pro Thr Ser Asn His Gly Pro Asp Ala Thr Glu Ala
65                  70                  75                  80

Glu Glu Asp Phe Val Asp Pro Trp Thr Val Gln Thr Ser Ser Ala Lys
            85                  90                  95
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Gly Ile Asp Tyr Asp Lys Leu Ile Val Arg Phe Gly Ser Ser Lys Ile
            100   105   110

Asp Lys Glu Leu Ile Asn Arg Ile Glu Arg Ala Thr Gly Gln Arg Pro
            115   120   125

His His Phe Leu Arg Arg Gly Ile Phe Phe Ser His Arg Asp Met Asn
    130   135   140

Gln Val Leu Asp Ala Tyr Glu Asn Lys Lys Pro Phe Tyr Leu Tyr Thr
145   150   155   160

Gly Arg Gly Pro Ser Ser Glu Ala Met His Val Gly His Leu Ile Pro
                165   170   175

Phe Ile Phe Thr Lys Trp Leu Gln Asp Val Phe Asn Val Pro Leu Val
                180   185   190

Ile Gln Met Thr Asp Asp Glu Lys Tyr Leu Trp Lys Asp Leu Thr Leu
            195   200   205

Asp Gln Ala Tyr Gly Asp Ala Val Glu Asn Ala Lys Asp Ile Ile Ala
    210   215   220

Cys Gly Phe Asp Ile Asn Lys Thr Phe Ile Phe Ser Asp Leu Asp Tyr
225   230   235   240

Met Gly Met Ser Ser Gly Phe Tyr Lys Asn Val Val Lys Ile Gln Lys
                245   250   255

His Val Thr Phe Asn Gln Val Lys Gly Ile Phe Gly Phe Thr Asp Ser
                260   265   270

Asp Cys Ile Gly Lys Ile Ser Phe Pro Ala Ile Gln Ala Ala Pro Ser
            275   280   285

Phe Ser Asn Ser Phe Pro Gln Ile Phe Arg Asp Arg Thr Asp Ile Gln
    290   295   300

Cys Leu Ile Pro Cys Ala Ile Asp Gln Asp Pro Tyr Phe Arg Met Thr
305   310   315   320

Arg Asp Val Ala Pro Arg Ile Gly Tyr Pro Lys Pro Ala Leu Leu His
                325   330   335

Ser Thr Phe Phe Pro Ala Leu Gln Gly Ala Gln Thr Lys Met Ser Ala
                340   345   350

Ser Asp Pro Asn Ser Ser Ile Phe Leu Thr Asp Thr Ala Lys Gln Ile
            355   360   365

Lys Thr Lys Val Asn Lys His Ala Phe Ser Gly Gly Arg Asp Thr Ile
    370   375   380

Glu Glu His Arg Gln Phe Gly Gly Asn Cys Asp Val Asp Val Ser Phe
385   390   395   400

Met Tyr Leu Thr Phe Phe Leu Glu Asp Asp Asp Lys Leu Glu Gln Ile
                405   410   415

Arg Lys Asp Tyr Thr Ser Gly Ala Met Leu Thr Gly Glu Leu Lys Lys
            420   425   430

```
Ala Leu Ile Glu Val Leu Gln Pro Leu Ile Ala Glu His Gln Ala Arg
    435                 440             445

Arg Lys Glu Val Thr Asp Glu Ile Val Lys Glu Phe Met Thr Pro Arg
    450             455             460

Lys Leu Ser Phe Asp Phe Gln Lys Leu Ala Ala Ala Leu Glu His His
465             470             475             480

His His His His
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<210> 11
<211> 4877
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (3428)..(4738)

<220>
<223> Description of Artificial Sequence: human mini
      TrpRS in pET20B

<400> 11
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cagcgtgacc gctacacttg ccagcgccct agcgcccgct cctttcgctt tcttcccttc  120

ctttctcgcc acgttcgccg gctttccccg tcaagctcta aatcgggggc tccctttagg  180

gttccgattt agtgctttac ggcacctcga ccccaaaaaa cttgattagg gtgatggttc  240

acgtagtggg ccatcgccct gatagacggt ttttcgccct ttgacgttgg agtccacgtt  300

ctttaatagt ggactcttgt tccaaactgg aacaacactc aaccctatct cggtctattc  360

ttttgattta taagggattt tgccgatttc ggcctattgg ttaaaaaatg agctgattta  420

acaaaaattt aacgcgaatt ttaacaaaat attaacgttt acaatttcag gtggcacttt  480

tcggggaaat gtgcgcggaa cccctatttg tttatttttc taaatacatt caaatatgta  540

tccgctcatg agacaataac cctgataaat gcttcaataa tattgaaaaa ggaagagtat  600

gagtattcaa catttccgtg tcgcccttat ccctttttt gcggcatttt gccttcctgt  660

ttttgctcac ccagaaacgc tggtgaaagt aaaagatgct gaagatcagt tgggtgcacg  720

agtgggttac atcgaactgg atctcaacag cggtaagatc cttgagagtt ttcgccccga  780

agaacgtttt ccaatgatga gcacttttaa agttctgcta tgtggcgcgg tattatcccg  840

tattgacgcc gggcaagagc aactcggtcg ccgcatacac tattctcaga atgacttggt  900

tgagtactca ccagtcacag aaaagcatct tacggatggc atgacagtaa gagaattatg  960

cagtgctgcc ataaccatga gtgataacac tgcggccaac ttacttctga caacgatcgg  1020
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aggaccgaag gagctaaccg cttttttgca caacatgggg gatcatgtaa ctcgccttga 1080

tcgttgggaa ccggagctga atgaagccat accaaacgac gagcgtgaca ccacgatgcc 1140

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ggcccttccg gctggctggt ttattgctga taaatctgga gccggtgagc gtgggtctcg 1320

cggtatcatt gcagcactgg ggccagatgg taagccctcc cgtatcgtag ttatctacac 1380

gacggggagt caggcaacta tggatgaacg aaatagacag atcgctgaga taggtgcctc 1440

actgattaag cattggtaac tgtcagacca agtttactca tatatacttt agattgattt 1500

aaaacttcat ttttaattta aaaggatcta ggtgaagatc cttttttgata atctcatgac 1560

caaaatccct taacgtgagt tttcgttcca ctgagcgtca gaccccgtag aaaagatcaa 1620

aggatcttct tgagatcctt tttttctgcg cgtaatctgc tgcttgcaaa caaaaaaacc 1680

accgctacca gcggtggttt gtttgccgga tcaagagcta ccaactcttt ttccgaaggt 1740

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accggataag cgcagcggt cgggctgaac ggggggttcg tgcacacagc ccagcttgga 1980

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cgctacgtga ctgggtcatg gctgcgcccc gacacccgcc aacacccgct gacgcgccct 2580

gacgggcttg tctgctcccg gcatccgctt acagacaagc tgtgaccgtc tccgggagct 2640

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cccgtggcca ggacccaacg ctgcccgaga tctcgatccc gcgaaattaa tacgactcac 3360

tataggga ccacaacggt ttccctctag aaataatttt gtttaacttt aagaaggaga 3420

```
tatacat atg agc tac aaa gct gcc gcg ggg gag gat tac aag gct gac   3469
        Met Ser Tyr Lys Ala Ala Ala Gly Glu Asp Tyr Lys Ala Asp
         1               5                  10

tgt cct cca ggg aac cca gca cct acc agt aat cat ggc cca gat gcc   3517
Cys Pro Pro Gly Asn Pro Ala Pro Thr Ser Asn His Gly Pro Asp Ala
 15              20              25                  30

aca gaa gct gaa gag gat ttt gtg gac cca tgg aca gta cag aca agc   3565
Thr Glu Ala Glu Glu Asp Phe Val Asp Pro Trp Thr Val Gln Thr Ser
             35                  40                  45

agt gca aaa ggc ata gac tac gat aag ctc att gtt cgg ttt gga agt   3613
Ser Ala Lys Gly Ile Asp Tyr Asp Lys Leu Ile Val Arg Phe Gly Ser
         50                  55                  60

agt aaa att gac aaa gag cta ata aac cga ata gag aga gcc acc ggc   3661
Ser Lys Ile Asp Lys Glu Leu Ile Asn Arg Ile Glu Arg Ala Thr Gly
         65                  70                  75

caa aga cca cac cac ttc ctg cgc aga ggc atc ttc ttc tca cac aga   3709
Gln Arg Pro His His Phe Leu Arg Arg Gly Ile Phe Phe Ser His Arg
         80                  85                  90

gat atg aat cag gtt ctt gat gcc tat gaa aat aag aag cca ttt tat   3757
Asp Met Asn Gln Val Leu Asp Ala Tyr Glu Asn Lys Lys Pro Phe Tyr
 95                  100                 105                 110

ctg tac acg ggc cgg ggc ccc tct tct gaa gca atg cat gta ggt cac   3805
Leu Tyr Thr Gly Arg Gly Pro Ser Ser Glu Ala Met His Val Gly His
             115                 120                 125

ctc att cca ttt att ttc aca aag tgg ctc cag gat gta ttt aac gtg   3853
Leu Ile Pro Phe Ile Phe Thr Lys Trp Leu Gln Asp Val Phe Asn Val
             130                 135                 140

ccc ttg gtc atc cag atg acg gat gac gag aag tat ctg tgg aag gac   3901
Pro Leu Val Ile Gln Met Thr Asp Asp Glu Lys Tyr Leu Trp Lys Asp
         145                 150                 155

ctg acc ctg gac cag gcc tat ggc gat gct gtt gag aat gcc aag gac   3949
Leu Thr Leu Asp Gln Ala Tyr Gly Asp Ala Val Glu Asn Ala Lys Asp
 160                 165                 170
```

```
atc atc gcc tgt ggc ttt gac atc aac aag act ttc ata ttc tct gac    3997
Ile Ile Ala Cys Gly Phe Asp Ile Asn Lys Thr Phe Ile Phe Ser Asp
175             180             185             190

ctg gac tac atg ggg atg agc tca ggt ttc tac aaa aat gtg gtg aag    4045
Leu Asp Tyr Met Gly Met Ser Ser Gly Phe Tyr Lys Asn Val Val Lys
                195             200             205

att caa aag cat gtt acc ttc aac caa gtg aaa ggc att ttc ggc ttc    4093
Ile Gln Lys His Val Thr Phe Asn Gln Val Lys Gly Ile Phe Gly Phe
                210             215             220

act gac agc gac tgc att ggg aag atc agt ttt cct gcc atc cag gct    4141
Thr Asp Ser Asp Cys Ile Gly Lys Ile Ser Phe Pro Ala Ile Gln Ala
            225             230             235

gct ccc tcc ttc agc aac tca ttc cca cag atc ttc cga gac agg acg    4189
Ala Pro Ser Phe Ser Asn Ser Phe Pro Gln Ile Phe Arg Asp Arg Thr
        240             245             250

gat atc cag tgc ctt atc cca tgt gcc att gac cag gat cct tac ttt    4237
Asp Ile Gln Cys Leu Ile Pro Cys Ala Ile Asp Gln Asp Pro Tyr Phe
255             260             265             270

aga atg aca agg gac gtc gcc ccc agg atc ggc tat cct aaa cca gcc    4285
Arg Met Thr Arg Asp Val Ala Pro Arg Ile Gly Tyr Pro Lys Pro Ala
                275             280             285

ctg ttg cac tcc acc ttc ttc cca gcc ctg cag ggc gcc cag acc aaa    4333
Leu Leu His Ser Thr Phe Phe Pro Ala Leu Gln Gly Ala Gln Thr Lys
                290             295             300

atg agt gcc agc gac cca aac tcc tcc atc ttc ctc acc gac acg gcc    4381
Met Ser Ala Ser Asp Pro Asn Ser Ser Ile Phe Leu Thr Asp Thr Ala
            305             310             315

aag cag atc aaa acc aag gtc aat aag cat gcg ttt tct gga ggg aga    4429
Lys Gln Ile Lys Thr Lys Val Asn Lys His Ala Phe Ser Gly Gly Arg
        320             325             330

gac acc atc gag gag cac agg cag ttt ggg ggc aac tgt gat gtg gac    4477
Asp Thr Ile Glu Glu His Arg Gln Phe Gly Gly Asn Cys Asp Val Asp
335             340             345             350

gtg tct ttc atg tac ctg acc ttc ttc ctc gag gac gac gac aag ctc    4525
Val Ser Phe Met Tyr Leu Thr Phe Phe Leu Glu Asp Asp Asp Lys Leu
                355             360             365

gag cag atc agg aag gat tac acc agc gga gcc atg ctc acc ggt gag    4573
Glu Gln Ile Arg Lys Asp Tyr Thr Ser Gly Ala Met Leu Thr Gly Glu
                370             375             380

ctc aag aag gca ctc ata gag gtt ctg cag ccc ttg atc gca gag cac    4621
Leu Lys Lys Ala Leu Ile Glu Val Leu Gln Pro Leu Ile Ala Glu His
            385             390             395

cag gcc cgg cgc aag gag gtc acg gat gag ata gtg aaa gag ttc atg    4669
Gln Ala Arg Arg Lys Glu Val Thr Asp Glu Ile Val Lys Glu Phe Met
        400             405             410
```

```
act ccc cgg aag ctg tcc ttc gac ttt cag aag ctt gcg gcc gca ctc   4717
Thr Pro Arg Lys Leu Ser Phe Asp Phe Gln Lys Leu Ala Ala Ala Leu
415             420             425             430

gag cac cac cac cac cac cac tgagatccgg ctgctaacaa agcccgaaag   4768
Glu His His His His His His
                435

gaagctgagt tggctgctgc caccgctgag caataactag cataacccct tggggcctct 4828

aaacgggtct tgaggggttt tttgctgaaa ggaggaacta tatccggat              4877
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<210> 12
<211> 437
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: human mini
      TrpRS in pET20B

<400> 12
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Pro Gly Asn Pro Ala Pro Thr Ser Asn His Gly Pro Asp Ala Thr Glu
                20                  25                  30

Ala Glu Glu Asp Phe Val Asp Pro Trp Thr Val Gln Thr Ser Ser Ala
        35                  40                  45

Lys Gly Ile Asp Tyr Asp Lys Leu Ile Val Arg Phe Gly Ser Ser Lys
    50                  55                  60

Ile Asp Lys Glu Leu Ile Asn Arg Ile Glu Arg Ala Thr Gly Gln Arg
 65                  70                  75                  80

Pro His His Phe Leu Arg Arg Gly Ile Phe Phe Ser His Arg Asp Met
                85                  90                  95

Asn Gln Val Leu Asp Ala Tyr Glu Asn Lys Lys Pro Phe Tyr Leu Tyr
            100                 105                 110

Thr Gly Arg Gly Pro Ser Ser Glu Ala Met His Val Gly His Leu Ile
            115                 120                 125

Pro Phe Ile Phe Thr Lys Trp Leu Gln Asp Val Phe Asn Val Pro Leu
        130                 135                 140

Val Ile Gln Met Thr Asp Asp Glu Lys Tyr Leu Trp Lys Asp Leu Thr
145                 150                 155                 160

Leu Asp Gln Ala Tyr Gly Asp Ala Val Glu Asn Ala Lys Asp Ile Ile
                165                 170                 175

Ala Cys Gly Phe Asp Ile Asn Lys Thr Phe Ile Phe Ser Asp Leu Asp
                180                 185                 190

Tyr Met Gly Met Ser Ser Gly Phe Tyr Lys Asn Val Val Lys Ile Gln
            195                 200                 205
```

```
Lys His Val Thr Phe Asn Gln Val Lys Gly Ile Phe Gly Phe Thr Asp
    210             215             220
```

```
Ser Asp Cys Ile Gly Lys Ile Ser Phe Pro Ala Ile Gln Ala Ala Pro
225             230             235             240
```

```
Ser Phe Ser Asn Ser Phe Pro Gln Ile Phe Arg Asp Arg Thr Asp Ile
            245             250             255
```

```
Gln Cys Leu Ile Pro Cys Ala Ile Asp Gln Asp Pro Tyr Phe Arg Met
        260             265             270
```

```
Thr Arg Asp Val Ala Pro Arg Ile Gly Tyr Pro Lys Pro Ala Leu Leu
        275             280             285
```

```
His Ser Thr Phe Phe Pro Ala Leu Gln Gly Ala Gln Thr Lys Met Ser
    290             295             300
```

```
Ala Ser Asp Pro Asn Ser Ser Ile Phe Leu Thr Asp Thr Ala Lys Gln
305             310             315             320
```

```
Ile Lys Thr Lys Val Asn Lys His Ala Phe Ser Gly Gly Arg Asp Thr
            325             330             335
```

```
Ile Glu Glu His Arg Gln Phe Gly Gly Asn Cys Asp Val Asp Val Ser
        340             345             350
```

```
Phe Met Tyr Leu Thr Phe Phe Leu Glu Asp Asp Asp Lys Leu Glu Gln
        355             360             365
```

```
Ile Arg Lys Asp Tyr Thr Ser Gly Ala Met Leu Thr Gly Glu Leu Lys
    370             375             380
```

```
Lys Ala Leu Ile Glu Val Leu Gln Pro Leu Ile Ala Glu His Gln Ala
385             390             395             400
```

```
Arg Arg Lys Glu Val Thr Asp Glu Ile Val Lys Glu Phe Met Thr Pro
            405             410             415
```

```
Arg Lys Leu Ser Phe Asp Phe Gln Lys Leu Ala Ala Ala Leu Glu His
        420             425             430
```

```
His His His His His
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<210> 13
<211> 4811
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (3428)..(4672)

<220>
<223> Description of Artificial Sequence: human
      supermini TrpRS in pET20B

<400> 13
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ctttctcgcc acgttcgccg gctttccccg tcaagctcta aatcgggggc tccctttagg 180

gttccgattt agtgctttac ggcacctcga ccccaaaaaa cttgattagg gtgatggttc 240

acgtagtggg ccatcgccct gatagacggt ttttcgccct ttgacgttgg agtccacgtt 300

ctttaatagt ggactcttgt tccaaactgg aacaacactc aaccctatct cggtctattc 360

ttttgattta taagggattt tgccgatttc ggcctattgg ttaaaaaatg agctgattta 420

acaaaaattt aacgcgaatt ttaacaaaat attaacgttt acaatttcag gtggcacttt 480

tcggggaaat gtgcgcggaa cccctatttg tttattttc taaatacatt caaatatgta 540

tccgctcatg agacaataac cctgataaat gcttcaataa tattgaaaaa ggaagagtat 600

gagtattcaa catttccgtg tcgcccttat tcccttttt gcggcatttt gccttcctgt 660

ttttgctcac ccagaaacgc tggtgaaagt aaaagatgct gaagatcagt tgggtgcacg 720

agtgggttac atcgaactgg atctcaacag cggtaagatc cttgagagtt ttcgccccga 780

agaacgtttt ccaatgatga gcactttaa agttctgcta tgtggcgcgg tattatcccg 840

tattgacgcc gggcaagagc aactcggtcg ccgcatacac tattctcaga atgacttggt 900

tgagtactca ccagtcacag aaaagcatct tacggatggc atgacagtaa gagaattatg 960

cagtgctgcc ataaccatga gtgataacac tgcggccaac ttacttctga caacgatcgg 1020

aggaccgaag gagctaaccg cttttttgca caacatgggg gatcatgtaa ctcgccttga 1080

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aaaacttcat ttttaattta aaaggatcta ggtgaagatc cttttttgata atctcatgac 1560

caaaatccct taacgtgagt tttcgttcca ctgagcgtca daccccgtag aaaagatcaa 1620

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accgctacca gcggtggttt gtttgccgga tcaagagcta ccaactcttt ttccgaaggt 1740

aactggcttc agcagagcgc agataccaaa tactgtcctt ctagtgtagc cgtagttagg 1800

ccaccacttc aagaactctg tagcaccgcc tacatacctc gctctgctaa tcctgttacc 1860

agtggctgct gccagtggcg ataagtcgtg tcttaccggg ttggactcaa gacgatagtt 1920

accggataag gcgcagcggt cgggctgaac ggggggttcg tgcacacagc ccagcttgga 1980

gcgaacgacc tacaccgaac tgagatacct acagcgtgag ctatgagaaa gcgccacgct 2040

tcccgaaggg agaaaggcgg acaggtatcc ggtaagcggc agggtcggaa caggagagcg 2100

cacgagggag cttccagggg gaaacgcctg gtatctttat agtcctgtcg ggtttcgcca 2160

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gcgcctgatg cggtattttc tccttacgca tctgtgcggt atttcacacc gcatatatgg 2460

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cgctacgtga ctgggtcatg gctgcgcccc gacacccgcc aacacccgct gacgcgccct 2580

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gcatgtgtca gaggttttca ccgtcatcac cgaaacgcgc gaggcagctg cggtaaagct 2700

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cccgtggcca ggacccaacg ctgcccgaga tctcgatccc gcgaaattaa tacgactcac 3360

tatagggaga ccacaacggt ttccctctag aaataatttt gtttaacttt aagaaggaga 3420

tatacat atg agt aat cat ggc cca gat gcc aca gaa gct gaa gag gat   3469
        Met Ser Asn His Gly Pro Asp Ala Thr Glu Ala Glu Glu Asp
        1   5   10

ttt gtg gac cca tgg aca gta cag aca agc agt gca aaa ggc ata gac   3517
Phe Val Asp Pro Trp Thr Val Gln Thr Ser Ser Ala Lys Gly Ile Asp
15   20   25   30

tac gat aag ctc att gtt cgg ttt gga agt agt aaa att gac aaa gag   3565
Tyr Asp Lys Leu Ile Val Arg Phe Gly Ser Ser Lys Ile Asp Lys Glu
            35   40   45

```
cta ata aac cga ata gag aga gcc acc ggc caa aga cca cac cac ttc     3613
Leu Ile Asn Arg Ile Glu Arg Ala Thr Gly Gln Arg Pro His His Phe
            50                  55                  60

ctg cgc aga ggc atc ttc ttc tca cac aga gat atg aat cag gtt ctt     3661
Leu Arg Arg Gly Ile Phe Phe Ser His Arg Asp Met Asn Gln Val Leu
            65                  70                  75

gat gcc tat gaa aat aag aag cca ttt tat ctg tac acg ggc cgg ggc     3709
Asp Ala Tyr Glu Asn Lys Lys Pro Phe Tyr Leu Tyr Thr Gly Arg Gly
        80                  85                  90

ccc tct tct gaa gca atg cat gta ggt cac ctc att cca ttt att ttc     3757
Pro Ser Ser Glu Ala Met His Val Gly His Leu Ile Pro Phe Ile Phe
     95                  100                 105                 110

aca aag tgg ctc cag gat gta ttt aac gtg ccc ttg gtc atc cag atg     3805
Thr Lys Trp Leu Gln Asp Val Phe Asn Val Pro Leu Val Ile Gln Met
                115                 120                 125

acg gat gac gag aag tat ctg tgg aag gac ctg acc ctg gac cag gcc     3853
Thr Asp Asp Glu Lys Tyr Leu Trp Lys Asp Leu Thr Leu Asp Gln Ala
            130                 135                 140

tat ggc gat gct gtt gag aat gcc aag gac atc atc gcc tgt ggc ttt     3901
Tyr Gly Asp Ala Val Glu Asn Ala Lys Asp Ile Ile Ala Cys Gly Phe
            145                 150                 155

gac atc aac aag act ttc ata ttc tct gac ctg gac tac atg ggg atg     3949
Asp Ile Asn Lys Thr Phe Ile Phe Ser Asp Leu Asp Tyr Met Gly Met
        160                 165                 170

agc tca ggt ttc tac aaa aat gtg gtg aag att caa aag cat gtt acc     3997
Ser Ser Gly Phe Tyr Lys Asn Val Val Lys Ile Gln Lys His Val Thr
175                 180                 185                 190

ttc aac caa gtg aaa ggc att ttc ggc ttc act gac agc gac tgc att     4045
Phe Asn Gln Val Lys Gly Ile Phe Gly Phe Thr Asp Ser Asp Cys Ile
                195                 200                 205

ggg aag atc agt ttt cct gcc atc cag gct gct ccc tcc ttc agc aac     4093
Gly Lys Ile Ser Phe Pro Ala Ile Gln Ala Ala Pro Ser Phe Ser Asn
            210                 215                 220

tca ttc cca cag atc ttc cga gac agg acg gat atc cag tgc ctt atc     4141
Ser Phe Pro Gln Ile Phe Arg Asp Arg Thr Asp Ile Gln Cys Leu Ile
            225                 230                 235

cca tgt gcc att gac cag gat cct tac ttt aga atg aca agg gac gtc     4189
Pro Cys Ala Ile Asp Gln Asp Pro Tyr Phe Arg Met Thr Arg Asp Val
        240                 245                 250

gcc ccc agg atc ggc tat cct aaa cca gcc ctg ttg cac tcc acc ttc     4237
Ala Pro Arg Ile Gly Tyr Pro Lys Pro Ala Leu Leu His Ser Thr Phe
255                 260                 265                 270

ttc cca gcc ctg cag ggc gcc cag acc aaa atg agt gcc agc gac cca     4285
Phe Pro Ala Leu Gln Gly Ala Gln Thr Lys Met Ser Ala Ser Asp Pro
            275                 280                 285
```

```
aac tcc tcc atc ttc ctc acc gac acg gcc aag cag atc aaa acc aag    4333
Asn Ser Ser Ile Phe Leu Thr Asp Thr Ala Lys Gln Ile Lys Thr Lys
            290                 295                 300

gtc aat aag cat gcg ttt tct gga ggg aga gac acc atc gag gag cac    4381
Val Asn Lys His Ala Phe Ser Gly Gly Arg Asp Thr Ile Glu Glu His
            305                 310                 315

agg cag ttt ggg ggc aac tgt gat gtg gac gtg tct ttc atg tac ctg    4429
Arg Gln Phe Gly Gly Asn Cys Asp Val Asp Val Ser Phe Met Tyr Leu
            320                 325                 330

acc ttc ttc ctc gag gac gac gac aag ctc gag cag atc agg aag gat    4477
Thr Phe Phe Leu Glu Asp Asp Asp Lys Leu Glu Gln Ile Arg Lys Asp
335                 340                 345                 350

tac acc agc gga gcc atg ctc acc ggt gag ctc aag aag gca ctc ata    4525
Tyr Thr Ser Gly Ala Met Leu Thr Gly Glu Leu Lys Lys Ala Leu Ile
                355                 360                 365

gag gtt ctg cag ccc ttg atc gca gag cac cag gcc cgg cgc aag gag    4573
Glu Val Leu Gln Pro Leu Ile Ala Glu His Gln Ala Arg Arg Lys Glu
                370                 375                 380

gtc acg gat gag ata gtg aaa gag ttc atg act ccc cgg aag ctg tcc    4621
Val Thr Asp Glu Ile Val Lys Glu Phe Met Thr Pro Arg Lys Leu Ser
            385                 390                 395

ttc gac ttt cag aag ctt gcg gcc gca ctc gag cac cac cac cac cac    4669
Phe Asp Phe Gln Lys Leu Ala Ala Ala Leu Glu His His His His His
            400                 405                 410

cac tgagatccgg ctgctaacaa agcccgaaag gaagctgagt tggctgctgc        4722
His
415

caccgctgag caataactag cataacccct tggggcctct aaacgggtct tgaggggttt 4782

tttgctgaaa ggaggaacta tatccggat                                   4811


<210> 14
<211> 415
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: human
      supermini TrpRS in pET20B

<400> 14
Met Ser Asn His Gly Pro Asp Ala Thr Glu Ala Glu Glu Asp Phe Val
  1               5                  10                  15

Asp Pro Trp Thr Val Gln Thr Ser Ser Ala Lys Gly Ile Asp Tyr Asp
             20                  25                  30

Lys Leu Ile Val Arg Phe Gly Ser Ser Lys Ile Asp Lys Glu Leu Ile
         35                  40                  45

Asn Arg Ile Glu Arg Ala Thr Gly Gln Arg Pro His His Phe Leu Arg
     50                  55                  60
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Arg Gly Ile Phe Phe Ser His Arg Asp Met Asn Gln Val Leu Asp Ala
65   70   75   80

Tyr Glu Asn Lys Lys Pro Phe Tyr Leu Tyr Thr Gly Arg Gly Pro Ser
                85   90   95

Ser Glu Ala Met His Val Gly His Leu Ile Pro Phe Ile Phe Thr Lys
            100   105   110

Trp Leu Gln Asp Val Phe Asn Val Pro Leu Val Ile Gln Met Thr Asp
        115   120   125

Asp Glu Lys Tyr Leu Trp Lys Asp Leu Thr Leu Asp Gln Ala Tyr Gly
    130   135   140

Asp Ala Val Glu Asn Ala Lys Asp Ile Ile Ala Cys Gly Phe Asp Ile
145   150   155   160

Asn Lys Thr Phe Ile Phe Ser Asp Leu Asp Tyr Met Gly Met Ser Ser
                165   170   175

Gly Phe Tyr Lys Asn Val Val Lys Ile Gln Lys His Val Thr Phe Asn
            180   185   190

Gln Val Lys Gly Ile Phe Gly Phe Thr Asp Ser Asp Cys Ile Gly Lys
        195   200   205

Ile Ser Phe Pro Ala Ile Gln Ala Ala Pro Ser Phe Ser Asn Ser Phe
    210   215   220

Pro Gln Ile Phe Arg Asp Arg Thr Asp Ile Gln Cys Leu Ile Pro Cys
225   230   235   240

Ala Ile Asp Gln Asp Pro Tyr Phe Arg Met Thr Arg Asp Val Ala Pro
            245   250   255

Arg Ile Gly Tyr Pro Lys Pro Ala Leu Leu His Ser Thr Phe Phe Pro
            260   265   270

Ala Leu Gln Gly Ala Gln Thr Lys Met Ser Ala Ser Asp Pro Asn Ser
        275   280   285

Ser Ile Phe Leu Thr Asp Thr Ala Lys Gln Ile Lys Thr Lys Val Asn
    290   295   300

Lys His Ala Phe Ser Gly Gly Arg Asp Thr Ile Glu Glu His Arg Gln
305   310   315   320

Phe Gly Gly Asn Cys Asp Val Asp Val Ser Phe Met Tyr Leu Thr Phe
                325   330   335

Phe Leu Glu Asp Asp Asp Lys Leu Glu Gln Ile Arg Lys Asp Tyr Thr
        340   345   350

Ser Gly Ala Met Leu Thr Gly Glu Leu Lys Lys Ala Leu Ile Glu Val
        355   360   365

Leu Gln Pro Leu Ile Ala Glu His Gln Ala Arg Arg Lys Glu Val Thr
    370   375   380

Asp Glu Ile Val Lys Glu Phe Met Thr Pro Arg Lys Leu Ser Phe Asp
385   390   395   400

Phe Gln Lys Leu Ala Ala Ala Leu Glu His His His His His
          405   410   415

<210> 15
<211> 4742
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (3428)..(4603)

<220>
<223> Description of Artificial Sequence: human minor
      Trp-RS fragment in pET20B

<400> 15
tggcgaatgg gacgcgccct gtagcggcgc attaagcgcg gcgggtgtgg tggttacgcg 60

cagcgtgacc gctacacttg ccagcgccct agcgcccgct cctttcgctt tcttcccttc 120

ctttctcgcc acgttcgccg gctttccccg tcaagctcta aatcgggggc tccctttagg 180

gttccgattt agtgctttac ggcacctcga ccccaaaaaa cttgattagg gtgatggttc 240

acgtagtggg ccatcgccct gatagacggt ttttcgccct ttgacgttgg agtccacgtt 300

ctttaatagt ggactcttgt tccaaactgg aacaacactc aaccctatct cggtctattc 360

ttttgattta agggatttt gccgatttc ggcctattgg ttaaaaaatg agctgattta 420

acaaaaattt aacgcgaatt ttaacaaaat attaacgttt acaatttcag gtggcacttt 480

tcggggaaat gtgcgcggaa ccccctatttg tttattttc taaatacatt caaatatgta 540

tccgctcatg agacaataac cctgataaat gcttcaataa tattgaaaaa ggaagagtat 600

gagtattcaa catttccgtg tcgcccttat ccctttttt gcggcatttt gccttcctgt 660

ttttgctcac ccagaaacgc tggtgaaagt aaaagatgct gaagatcagt tgggtgcacg 720

agtgggttac atcgaactgg atctcaacag cggtaagatc cttgagagtt ttcgccccga 780

agaacgtttt ccaatgatga gcacttttaa agttctgcta tgtggcgcgg tattatcccg 840

tattgacgcc gggcaagagc aactcggtcg ccgcatacac tattctcaga atgacttggt 900

tgagtactca ccagtcacag aaaagcatct tacggatggc atgacagtaa gagaattatg 960

cagtgctgcc ataaccatga gtgataacac tgcggccaac ttacttctga caacgatcgg 1020

aggaccgaag gagctaaccg cttttttgca acatgggg gatcatgtaa ctcgccttga 1080

tcgttgggaa ccggagctga atgaagccat accaaacgac gagcgtgaca ccacgatgcc 1140

tgcagcaatg gcaacaacgt tgcgcaaact attaactggc gaactactta ctctagcttc 1200

ccggcaacaa ttaatagact ggatggaggc ggataaagtt gcaggaccac ttctgcgctc 1260

ggcccttccg gctggctggt ttattgctga taaatctgga gccggtgagc gtgggtctcg 1320

cggtatcatt gcagcactgg ggccagatgg taagccctcc cgtatcgtag ttatctacac 1380

gacggggagt caggcaacta tggatgaacg aaatagacag atcgctgaga taggtgcctc 1440

actgattaag cattggtaac tgtcagacca agtttactca tatatacttt agattgattt 1500

aaaacttcat ttttaattta aaaggatcta ggtgaagatc cttttttgata atctcatgac 1560

caaaatccct taacgtgagt tttcgttcca ctgagcgtca gaccccgtag aaaagatcaa 1620

aggatcttct tgagatcctt tttttctgcg cgtaatctgc tgcttgcaaa caaaaaaacc 1680

accgctacca gcggtggttt gtttgccgga tcaagagcta ccaactcttt ttccgaaggt 1740

aactggcttc agcagagcgc agataccaaa tactgtcctt ctagtgtagc cgtagttagg 1800

ccaccacttc aagaactctg tagcaccgcc tacatacctc gctctgctaa tcctgttacc 1860

agtggctgct gccagtggcg ataagtcgtg tcttaccggg ttggactcaa gacgatagtt 1920

accggataag gcgcagcggt cgggctgaac ggggggttcg tgcacacagc ccagcttgga 1980

gcgaacgacc tacaccgaac tgagatacct acagcgtgag ctatgagaaa gcgccacgct 2040

tcccgaaggg agaaaggcgg acaggtatcc ggtaagcggc agggtcggaa caggagagcg 2100

cacgagggag cttccagggg gaaacgcctg gtatctttat agtcctgtcg ggtttcgcca 2160

cctctgactt gagcgtcgat ttttgtgatg ctcgtcaggg gggcggagcc tatggaaaaa 2220

cgccagcaac gcggcctttt tacggttcct ggccttttgc tggccttttg ctcacatgtt 2280

ctttcctgcg ttatcccctg attctgtgga taaccgtatt accgcctttg agtgagctga 2340

taccgctcgc cgcagccgaa cgaccgagcg cagcgagtca gtgagcgagg aagcggaaga 2400

gcgcctgatg cggtattttc tccttacgca tctgtgcggt atttcacacc gcatatatgg 2460

tgcactctca gtacaatctg ctctgatgcc gcatagttaa gccagtatac actccgctat 2520

cgctacgtga ctgggtcatg gctgcgcccc gacacccgcc aacacccgct gacgcgccct 2580

gacgggcttg tctgctcccg gcatccgctt acagacaagc tgtgaccgtc tccgggagct 2640

gcatgtgtca gaggttttca ccgtcatcac cgaaacgcgc gaggcagctg cggtaaagct 2700

catcagcgtg gtcgtgaagc gattcacaga tgtctgcctg ttcatccgcg tccagctcgt 2760

tgagtttctc cagaagcgtt aatgtctggc ttctgataaa gcgggccatg ttaagggcgg 2820

ttttttcctg tttggtcact gatgcctccg tgtaaggggg atttctgttc atggggggtaa 2880

tgataccgat gaaacgagag aggatgctca cgatacgggt tactgatgat gaacatgccc 2940

ggttactgga acgttgtgag ggtaaacaac tggcggtatg gatgcggcgg gaccagagaa 3000

aaatcactca gggtcaatgc cagcgcttcg ttaatacaga tgtaggtgtt ccacagggta 3060

gccagcagca tcctgcgatg cagatccgga acataatggt gcagggcgct gacttccgcg 3120

tttccagact ttacgaaaca cggaaaccga agaccattca tgttgttgct caggtcgcag 3180

acgttttgca gcagcagtcg cttcacgttc gctcgcgtat cggtgattca ttctgctaac 3240

cagtaaggca accccgccag cctagccggg tcctcaacga caggagcacg atcatgcgca 3300

cccgtggcca ggacccaacg ctgcccgaga tctcgatccc gcgaaattaa tacgactcac 3360

tatagggaga ccacaacggt ttccctctag aaataatttt gtttaacttt aagaaggaga 3420

tatacat atg agt gca aaa ggc ata gac tac gat aag ctc att gtt cgg   3469
        Met Ser Ala Lys Gly Ile Asp Tyr Asp Lys Leu Ile Val Arg
        1   5   10

ttt gga agt agt aaa att gac aaa gag cta ata aac cga ata gag aga   3517
Phe Gly Ser Ser Lys Ile Asp Lys Glu Leu Ile Asn Arg Ile Glu Arg
15   20   25   30

gcc acc ggc caa aga cca cac cac ttc ctg cgc aga ggc atc ttc ttc   3565
Ala Thr Gly Gln Arg Pro His His Phe Leu Arg Arg Gly Ile Phe Phe
                35   40   45

tca cac aga gat atg aat cag gtt ctt gat gcc tat gaa aat aag aag   3613
Ser His Arg Asp Met Asn Gln Val Leu Asp Ala Tyr Glu Asn Lys Lys
            50   55   60

cca ttt tat ctg tac acg ggc cgg ggc ccc tct tct gaa gca atg cat   3661
Pro Phe Tyr Leu Tyr Thr Gly Arg Gly Pro Ser Ser Glu Ala Met His
            65   70   75

gta ggt cac ctc att cca ttt att ttc aca aag tgg ctc cag gat gta   3709
Val Gly His Leu Ile Pro Phe Ile Phe Thr Lys Trp Leu Gln Asp Val
        80   85   90

ttt aac gtg ccc ttg gtc atc cag atg acg gat gac gag aag tat ctg   3757
Phe Asn Val Pro Leu Val Ile Gln Met Thr Asp Asp Glu Lys Tyr Leu
95   100   105   110

tgg aag gac ctg acc ctg gac cag gcc tat ggc gat gct gtt gag aat   3805
Trp Lys Asp Leu Thr Leu Asp Gln Ala Tyr Gly Asp Ala Val Glu Asn
                115   120   125

gcc aag gac atc atc gcc tgt ggc ttt gac atc aac aag act ttc ata   3853
Ala Lys Asp Ile Ile Ala Cys Gly Phe Asp Ile Asn Lys Thr Phe Ile
                130   135   140

ttc tct gac ctg gac tac atg ggg atg agc tca ggt ttc tac aaa aat   3901
Phe Ser Asp Leu Asp Tyr Met Gly Met Ser Ser Gly Phe Tyr Lys Asn
            145   150   155

gtg gtg aag att caa aag cat gtt acc ttc aac caa gtg aaa ggc att   3949
Val Val Lys Ile Gln Lys His Val Thr Phe Asn Gln Val Lys Gly Ile
        160   165   170

ttc ggc ttc act gac agc gac tgc att ggg aag atc agt ttt cct gcc   3997
Phe Gly Phe Thr Asp Ser Asp Cys Ile Gly Lys Ile Ser Phe Pro Ala
175   180   185   190

```
atc cag gct gct ccc tcc ttc agc aac tca ttc cca cag atc ttc cga   4045
Ile Gln Ala Ala Pro Ser Phe Ser Asn Ser Phe Pro Gln Ile Phe Arg
            195                 200                 205

gac agg acg gat atc cag tgc ctt atc cca tgt gcc att gac cag gat   4093
Asp Arg Thr Asp Ile Gln Cys Leu Ile Pro Cys Ala Ile Asp Gln Asp
            210                 215                 220

cct tac ttt aga atg aca agg gac gtc gcc ccc agg atc ggc tat cct   4141
Pro Tyr Phe Arg Met Thr Arg Asp Val Ala Pro Arg Ile Gly Tyr Pro
            225                 230                 235

aaa cca gcc ctg ttg cac tcc acc ttc ttc cca gcc ctg cag ggc gcc   4189
Lys Pro Ala Leu Leu His Ser Thr Phe Phe Pro Ala Leu Gln Gly Ala
    240                 245                 250

cag acc aaa atg agt gcc agc gac cca aac tcc tcc atc ttc ctc acc   4237
Gln Thr Lys Met Ser Ala Ser Asp Pro Asn Ser Ser Ile Phe Leu Thr
255                 260                 265                 270

gac acg gcc aag cag atc aaa acc aag gtc aat aag cat gcg ttt tct   4285
Asp Thr Ala Lys Gln Ile Lys Thr Lys Val Asn Lys His Ala Phe Ser
            275                 280                 285

gga ggg aga gac acc atc gag gag cac agg cag ttt ggg ggc aac tgt   4333
Gly Gly Arg Asp Thr Ile Glu Glu His Arg Gln Phe Gly Gly Asn Cys
            290                 295                 300

gat gtg gac gtg tct ttc atg tac ctg acc ttc ttc ctc gag gac gac   4381
Asp Val Asp Val Ser Phe Met Tyr Leu Thr Phe Phe Leu Glu Asp Asp
            305                 310                 315

gac aag ctc gag cag atc agg aag gat tac acc agc gga gcc atg ctc   4429
Asp Lys Leu Glu Gln Ile Arg Lys Asp Tyr Thr Ser Gly Ala Met Leu
            320                 325                 330

acc ggt gag ctc aag aag gca ctc ata gag gtt ctg cag ccc ttg atc   4477
Thr Gly Glu Leu Lys Lys Ala Leu Ile Glu Val Leu Gln Pro Leu Ile
335                 340                 345                 350

gca gag cac cag gcc cgg cgc aag gag gtc acg gat gag ata gtg aaa   4525
Ala Glu His Gln Ala Arg Arg Lys Glu Val Thr Asp Glu Ile Val Lys
            355                 360                 365

gag ttc atg act ccc cgg aag ctg tcc ttc gac ttt cag aag ctt gcg   4573
Glu Phe Met Thr Pro Arg Lys Leu Ser Phe Asp Phe Gln Lys Leu Ala
            370                 375                 380

gcc gca ctc gag cac cac cac cac cac cac tgagatccgg ctgctaacaa   4623
Ala Ala Leu Glu His His His His His His
    385                 390

agcccgaaag gaagctgagt tggctgctgc caccgctgag caataactag cataacccct 4683

tggggcctct aaacgggtct tgaggggttt tttgctgaaa ggaggaacta tatccggat  4742
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<210> 16
<211> 392
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: human minor
     TrpRS fragment in pET20B

<400> 16
Met Ser Ala Lys Gly Ile Asp Tyr Asp Lys Leu Ile Val Arg Phe Gly
 1   5   10   15

Ser Ser Lys Ile Asp Lys Glu Leu Ile Asn Arg Ile Glu Arg Ala Thr
            20   25   30

Gly Gln Arg Pro His His Phe Leu Arg Arg Gly Ile Phe Phe Ser His
        35   40   45

Arg Asp Met Asn Gln Val Leu Asp Ala Tyr Glu Asn Lys Lys Pro Phe
    50   55   60

Tyr Leu Tyr Thr Gly Arg Gly Pro Ser Ser Glu Ala Met His Val Gly
65   70   75   80

His Leu Ile Pro Phe Ile Phe Thr Lys Trp Leu Gln Asp Val Phe Asn
                85   90   95

Val Pro Leu Val Ile Gln Met Thr Asp Asp Glu Lys Tyr Leu Trp Lys
            100   105   110

Asp Leu Thr Leu Asp Gln Ala Tyr Gly Asp Ala Val Glu Asn Ala Lys
        115   120   125

Asp Ile Ile Ala Cys Gly Phe Asp Ile Asn Lys Thr Phe Ile Phe Ser
    130   135   140

Asp Leu Asp Tyr Met Gly Met Ser Ser Gly Phe Tyr Lys Asn Val Val
145   150   155   160

Lys Ile Gln Lys His Val Thr Phe Asn Gln Val Lys Gly Ile Phe Gly
                165   170   175

Phe Thr Asp Ser Asp Cys Ile Gly Lys Ile Ser Phe Pro Ala Ile Gln
            180   185   190

Ala Ala Pro Ser Phe Ser Asn Ser Phe Pro Gln Ile Phe Arg Asp Arg
        195   200   205

Thr Asp Ile Gln Cys Leu Ile Pro Cys Ala Ile Asp Gln Asp Pro Tyr
    210   215   220

Phe Arg Met Thr Arg Asp Val Ala Pro Arg Ile Gly Tyr Pro Lys Pro
225   230   235   240

Ala Leu Leu His Ser Thr Phe Phe Pro Ala Leu Gln Gly Ala Gln Thr
                245   250   255

Lys Met Ser Ala Ser Asp Pro Asn Ser Ser Ile Phe Leu Thr Asp Thr
            260   265   270

Ala Lys Gln Ile Lys Thr Lys Val Asn Lys His Ala Phe Ser Gly Gly
        275   280   285

Arg Asp Thr Ile Glu Glu His Arg Gln Phe Gly Gly Asn Cys Asp Val
    290   295   300

Asp Val Ser Phe Met Tyr Leu Thr Phe Phe Leu Glu Asp Asp Asp Lys
305   310   315   320

Leu Glu Gln Ile Arg Lys Asp Tyr Thr Ser Gly Ala Met Leu Thr Gly
                325   330   335

Glu Leu Lys Lys Ala Leu Ile Glu Val Leu Gln Pro Leu Ile Ala Glu
            340   345   350

His Gln Ala Arg Arg Lys Glu Val Thr Asp Glu Ile Val Lys Glu Phe
        355   360   365

Met Thr Pro Arg Lys Leu Ser Phe Asp Phe Gln Lys Leu Ala Ala Ala
    370   375   380

Leu Glu His His His His His His
385   390

<210> 17
<211> 6
<212> PRT
<213> Homo sapiens

<400> 17
Glu Leu Arg Val Ser Tyr
  1   5

<210> 18
<211> 6
<212> PRT
<213> Escherichia coli

<400> 18
Glu Thr Val Gln Glu Trp
  1   5

<210> 19
<211> 9
<212> PRT
<213> Homo sapiens

<400> 19
Ser Ala Lys Glu Leu Arg Cys Gln Cys
  1   5

<210> 20
<211> 11
<212> PRT
<213> Homo sapiens

<400> 20
Ala Ser Val Ala Thr Glu Leu Arg Cys Gln Cys
 1   5   10

<210> 21
<211> 7
<212> PRT
<213> Homo sapiens

<400> 21
Ala Glu Leu Arg Cys Gln Cys
 1   5

<210> 22
<211> 58
<212> PRT
<213> Homo sapiens

<400> 22
Gly Asp Glu Lys Lys Ala Lys Glu Lys Ile Glu Lys Lys Gly Glu Lys
 1   5   10   15

Lys Glu Lys Lys Gln Gln Ser Ile Ala Gly Ser Ala Asp Ser Lys Pro
                20   25   30

Ile Asp Val Ser Arg Leu Asp Leu Arg Ile Gly Cys Ile Ile Thr Ala
            35   40   45

Arg Lys His Pro Asp Ala Asp Ser Leu Tyr
        50   55

<210> 23
<211> 58
<212> PRT
<213> Homo sapiens

<400> 23
Pro Ala Leu Lys Lys Leu Ala Ser Ala Ala Tyr Pro Asp Pro Ser Lys
 1   5   10   15

Gln Lys Pro Met Ala Lys Gly Pro Ala Lys Asn Ser Glu Pro Glu Glu
                20   25   30

Val Ile Pro Ser Arg Leu Asp Ile Arg Val Gly Lys Ile Ile Thr Val
            35   40   45

Glu Lys His Pro Asp Ala Asp Ser Leu Tyr
        50   55

<210> 24
<211> 7
<212> PRT
<213> Homo sapiens

<400> 24
Arg Val Gly Lys Ile Ile Thr
 1   5

<210> 25
<211> 7
<212> PRT
<213> Homo sapiens

<400> 25
Arg Ile Gly Cys Ile Ile Thr
 1   5

<210> 26
<211> 7
<212> PRT
<213> Homo sapiens

<400> 26
Arg Ile Gly Arg Ile Ile Thr
 1   5

<210> 27
<211> 7
<212> PRT
<213> Caenorhabditis elegans

<400> 27
Arg Val Gly Arg Ile Ile Lys
 1   5

<210> 28
<211> 7
<212> PRT
<213> Saccharomyces cerevisiae

<400> 28
Arg Val Gly Phe Ile Gln Lys
 1   5

<210> 29
<211> 7
<212> PRT
<213> Bos taurus

<400> 29
Arg Val Gly Lys Val Ile Ser
 1   5

<210> 30
<211> 7
<212> PRT
<213> Mus musculus

<400> 30

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Arg Ile Gly Cys Ile Val Thr
 1               5
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```
<210> 31
<211> 7
<212> PRT
<213> Mesocricetus auratus
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```
<400> 31
Arg Ile Gly Arg Ile Val Thr
 1               5
```

```
<210> 32
<211> 7
<212> PRT
<213> Ovis aries
```

```
<400> 32
Arg Ile Gly Cys Ile Ile Thr
 1               5
```

```
<210> 33
<211> 7
<212> PRT
<213> Calcarea sp.
```

```
<400> 33
Arg Ile Gly Arg Ile Thr Ser
 1               5
```

```
<210> 34
<211> 7
<212> PRT
<213> A. aeolicus
```

```
<400> 34
Arg Val Ala Lys Val Leu Ser
 1               5
```

```
<210> 35
<211> 7
<212> PRT
<213> Escherichia coli
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```
<400> 35
Arg Val Gly Lys Ile Val Glu
 1               5
```

```
<210> 36
<211> 7
<212> PRT
<213> Escherichia coli
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```
<400> 36
Arg Val Ala Leu Ile Glu Asn
 1               5
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<210> 37
<211> 7
<212> PRT
<213> Haemophilus influenzae

<400> 37
Arg Val Ala Lys Val Leu Lys
 1   5

<210> 38
<211> 7
<212> PRT
<213> Bacillus subtilis

<400> 38
Arg Val Ala Glu Val Ile Glu
 1   5

<210> 39
<211> 7
<212> PRT
<213> B. stearothermophilus

<400> 39
Arg Val Ala Glu Val Val Gln
 1   5

<210> 40
<211> 7
<212> PRT
<213> Thermus thermophilus

<400> 40
Arg Val Ala Glu Val Leu Ala
 1   5

<210> 41
<211> 6
<212> PRT
<213> Escherichia coli

<400> 41
Val Gly Glu Val Val Glu
 1   5

<210> 42
<211> 6
<212> PRT
<213> Bacillus subtilis

<400> 42
Ile Gly His Val Leu Glu
 1   5

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<210> 43
<211> 6
<212> PRT
<213> Synechococcus sp.

<400> 43
Val Gly Arg Val Leu Glu
 1               5


<210> 44
<211> 6
<212> PRT
<213> Thermus thermophilus

<400> 44
Phe Ala Arg Val Leu Glu
 1               5


<210> 45
<211> 85
<212> PRT
<213> Homo sapiens

<400> 45
Met Ser Tyr Lys Ala Ala Ala Gly Glu Asp Tyr Lys Ala Asp Cys Pro
 1               5                  10                  15

Pro Gly Asn Pro Ala Pro Thr Ser Asn His Gly Pro Asp Ala Thr Glu
                20                  25                  30

Ala Glu Glu Asp Phe Val Asp Pro Trp Thr Val Gln Thr Ser Ser Ala
            35                  40                  45

Lys Gly Ile Asp Tyr Asp Lys Leu Ile Val Arg Phe Gly Ser Ser Lys
        50                  55                  60

Ile Asp Lys Glu Leu Ile Asn Arg Ile Glu Arg Ala Thr Gly Gln Arg
 65                  70                  75                  80

Pro His His Phe Leu
                85


<210> 46
<211> 85
<212> PRT
<213> Bos taurus

<400> 46
Thr Ser Tyr Lys Ala Ala Thr Gly Glu Asp Tyr Lys Val Asp Cys Pro
 1               5                  10                  15

Pro Gly Asp Pro Ala Pro Glu Ser Gly Glu Gly Leu Asp Ala Thr Glu
                20                  25                  30

Ala Asp Glu Asp Phe Val Asp Pro Trp Thr Val Gln Thr Ser Ser Ala
            35                  40                  45

Lys Gly Ile Asp Tyr Asp Lys Leu Ile Val Arg Phe Gly Ser Ser Lys
        50                  55                  60
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Ile Asp Lys Glu Leu Val Asn Arg Ile Glu Arg Ala Thr Gly Gln Arg
 65                  70                  75                      80

Pro His Arg Phe Leu
                 85


<210> 47
<211> 85
<212> PRT
<213> Mus musculus

<400> 47
Met Ser Tyr Lys Ala Ala Met Gly Glu Glu Tyr Lys Ala Gly Cys Pro
  1               5                  10                      15

Pro Gly Asn Pro Thr Ala Gly Arg Asn Cys Asp Ser Asp Ala Thr Lys
               20                  25                  30

Ala Ser Glu Asp Phe Val Asp Pro Trp Thr Val Arg Thr Ser Ser Ala
             35                  40                  45

Lys Gly Ile Asp Tyr Asp Lys Leu Ile Val Gln Pro Gly Ser Ser Lys
         50                  55                  60

Ile Asp Lys Glu Leu Ile Asn Arg Ile Glu Arg Ala Thr Gly Gln Arg
 65                  70                  75                      80

Pro His Arg Phe Leu
                 85


<210> 48
<211> 85
<212> PRT
<213> Oryctolagus cuniculus

<400> 48
Thr Ser Tyr Lys Glu Ala Met Gly Glu Asp Tyr Lys Ala Asp Cys Pro
  1               5                  10                      15

Pro Gly Asn Ser Thr Pro Asp Ser His Gly Pro Asp Glu Ala Val Asp
               20                  25                  30

Asp Lys Glu Asp Phe Val Asp Pro Trp Thr Val Arg Thr Ser Ser Ala
             35                  40                  45

Lys Gly Ile Asp Tyr Asp Lys Leu Ile Val Gln Phe Gly Ser Ser Lys
         50                  55                  60

Ile Asp Lys Glu Leu Val Asn Arg Ile Glu Arg Ala Thr Gly Gln Arg
 65                  70                  75                      80

Pro His Arg Phe Leu
                 85
```

<210> 49
<211> 86
<212> PRT
<213> Homo sapiens

<400> 49
Ile Ser Tyr Gln Gly Arg Ile Pro Tyr Pro Arg Pro Gly Thr Cys Pro
 1   5   10   15

Gly Gly Ala Phe Thr Pro Asn Met Arg Thr Thr Lys Glu Phe Pro Asp
                20   25   30

Asp Val Val Thr Phe Ile Arg Asn His Pro Leu Met Tyr Asn Ser Ile
            35   40   45

Tyr Pro Ile His Lys Arg Pro Leu Ile Val Arg Ile Gly Thr Asp Tyr
        50   55   60

Lys Tyr Thr Lys Ile Ala Val Asp Arg Val Asn Ala Ala Asp Gly Arg
65   70   75   80

Tyr His Val Leu Phe Leu
                85

<210> 50
<211> 86
<212> PRT
<213> Mus musculus

<400> 50
Ile Ser Tyr Gln Gly Arg Ile Pro Tyr Pro Arg Pro Gly Thr Cys Pro
 1   5   10   15

Gly Gly Ala Phe Thr Pro Asn Met Arg Thr Thr Lys Asp Phe Pro Asp
                20   25   30

Asp Val Val Thr Phe Ile Arg Asn His Pro Leu Met Tyr Asn Ser Ile
            35   40   45

Ser Pro Ile His Arg Arg Pro Leu Ile Val Arg Ile Gly Thr Asp Tyr
        50   55   60

Lys Tyr Thr Lys Ile Ala Val Asp Arg Val Asn Ala Ala Asp Gly Arg
65   70   75   80

Tyr His Val Leu Phe Leu
                85

<210> 51
<211> 46
<212> PRT
<213> Homo sapiens

<400> 51
Ala Ala Ala Gly Glu Asp Tyr Lys Ala Asp Cys Pro Pro Gly Asn Pro
 1   5   10   15

Ala Pro Thr Ser Asn His Gly Pro Asp Ala Thr Glu Ala Glu Glu Asp
                20   25   30

```
Phe Val Asp Pro Trp Thr Val Gln Thr Ser Ser Ala Lys Gly
        35                  40                  45
```

<210> 52
<211> 46
<212> PRT
<213> Bos taurus

<400> 52
```
Ala Ala Thr Gly Glu Asp Tyr Lys Val Asp Cys Pro Pro Gly Asp Pro
  1               5                  10                  15

Ala Pro Glu Ser Gly Glu Gly Leu Asp Ala Thr Glu Ala Asp Glu Asp
            20                  25                  30

Phe Val Asp Pro Trp Thr Val Gln Thr Ser Ser Ala Lys Gly
        35                  40                  45
```

<210> 53
<211> 46
<212> PRT
<213> Mus musculus

<400> 53
```
Ala Ala Met Gly Glu Glu Tyr Lys Ala Gly Cys Pro Pro Gly Asn Pro
  1               5                  10                  15

Thr Ala Gly Arg Asn Cys Asp Ser Asp Ala Thr Lys Ala Ser Glu Asp
            20                  25                  30

Phe Val Asp Pro Trp Thr Val Arg Thr Ser Ser Ala Lys Gly
        35                  40                  45
```

<210> 54
<211> 46
<212> PRT
<213> Oryctolagus cuniculus

<400> 54
```
Glu Ala Met Gly Glu Asp Tyr Lys Ala Asp Cys Pro Pro Gly Asn Ser
  1               5                  10                  15

Thr Pro Asp Ser His Gly Pro Asp Glu Ala Val Asp Asp Lys Glu Asp
            20                  25                  30

Phe Val Asp Pro Trp Thr Val Arg Thr Ser Ser Ala Lys Gly
        35                  40                  45
```

<210> 55
<211> 41
<212> PRT
<213> Mus musculus

<400> 55
```
Ala Phe Ala Gly Glu Asp Phe Lys Val Asp Ile Pro Glu Thr His Gly
  1               5                  10                  15
```

Gly Glu Gly Thr Glu Asp Glu Ile Asp Asp Glu Tyr Glu Gly Asp Trp
          20   25   30

Ser Asn Ser Ser Ser Ser Thr Ser Gly
          35   40

<210> 56
<211> 5
<212> PRT
<213> Homo sapiens

<400> 56
Met Gly Asp Ala Pro
  1   5

<210> 57
<211> 5
<212> PRT
<213> Homo sapiens

<400> 57
Ser Asn His Gly Pro
  1   5

<210> 58
<211> 5
<212> PRT
<213> Homo sapiens

<400> 58
Ser Ala Lys Gly Ile
  1   5

  1

  1